



FEATURES	Location/Qualifiers
source	1. . . 2007
	/organism="Homo sapiens"
gene	/db_xref="taxon:9606"
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	103. . . 1512
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	/protein_id="AAB52993_1"
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	/translation="MPIRALTCISDFDHSDRDAATHGIFTPHIOLISETETAPSRTFCRQIVGKRITINKFLDIAQEEENVLDREFFLNEDNRAQISQDKERKRSQVLDILRQYIENNAVATSLQQDNEALGAEMLCSITLKKQYIIEQDENTKQOEAEGLRSRNMKTMQIELLQSOPEVEREMDVGUGSAVEDLAUCVSIKYEENKEARKASGRVADKURKDESSRSKLTQYISELDAKLELSRAKDLQSDADEKLMSPRDSQHTRNLLPPVASETDRVLYESPAPEVNEVNLKRSRQDIDMUTDPPARPSQHGYVKECLEKESPIODVPKKCKGRKESDLSLGQSCAGEPDEELVGAAPPFIRNAIGOKQPKRPSSESSESKDVRGFDGIGGRKFIOTDTVMIRPLPVPKPKVKVORV
BASE COUNT	517 a 518 c 558 g 414 t
ORIGIN	
Query Match	100.0%; Score 2007; DB 9; Length 2007;
Best Local Similarity	100.0%; Pred. No. 0;
Matches	2007; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 GTCGGGTGGAGCCAAATTGAAAGCAAGGGAGGGGGGGCGCTTACGAGCCGGACCTGT 60
Db	1 GTCGGGTGGAGCCAAATTGAAAGCAAGGGAGGGGGGGCGCTTACGAGCCGGACCTGT 60
QY	61 AGCAGTTCCTTGCTGCTGGCCCTTGTAGCTTCAGTCGCTATCGTGCCTG 120
Db	61 AGCAGTTCCTTGCTGCTGGCCCTTGTAGCTTCAGTCGCTATCGTGCCTG 120
QY	121 TGCAGTATCTGCCTGGACTTCCTGAGTCATCCGAGCTGGCCGCATCGGGC 180
Db	121 TGCAGTATCTGCCTGGACTTCCTGAGTCATCCGAGCTGGCCGCATCGGGC 180
QY	181 CACACCTTCATCTGCACTGCTTAATTGAGTCCTTGTAGACAGCACCAGTGGACCTGC 240
Db	181 CACACCTTCATCTGCACTGCTTAATTGAGTCCTTGTAGACAGCACCAGTGGACCTGC 240
QY	241 CCGCAGTGGCCGAAACCAAGGTTGCGCAAAAGAACCTTATCAATAGCTCTTGTACCT 300
Db	241 CCGCAGTGGCCGAAACCAAGGTTGCGCAAAAGAACCTTATCAATAGCTCTTGTACCT 300
QY	301 GCCCAGGAGGAGGAATGTCCTGGATGAGAAATTCTAAGAATGACTGGACAATGTC 360
Db	301 GCCCAGGAGGAGGAATGTCCTGGATGAGAAATTCTAAGAATGACTGGACAATGTC 360
QY	361 AGGCCCCAGCTTCCAGAAAGAACAGAGCAGACAGCCAGGTCTATCGACACT 420
Db	361 AGGCCCCAGCTTCCAGAAAGAACAGAGCAGACAGCCAGGTCTATCGACACT 420
QY	421 CTCGGGGATACCGTGGAGAAGCCAGCACTGCTACTGTGTGTTATCTGGCCCTGGC 480
Db	421 CTCGGGGATACCGTGGAGAAGCCAGCACTGCTACTGTGTGTTATCTGGCCCTGGC 480
QY	481 AAGGCCAGATGCTGCTCCACACTGAAAGCAGATGACTTGTAGCCAGCAG 540
Db	481 AAGGCCAGATGCTGCTCCACACTGAAAGCAGATGACTTGTAGCCAGCAG 540
QY	541 GATGAGACCAACCAAGGAGGAGGGGGGGGGCTCAGGAGCAGATGAGACAT 600
Db	541 GATGAGACCAACCAAGGAGGAGGGGGGGGGCTCAGGAGCAGATGAGACAT 600
QY	601 GAGCAGAGTGGCTTCTACTCGAGGAGCCAGCTCCCTGAGGTGGAGGAGATGCCAGAC 660
Db	601 GAGCAGAGTGGCTTCTACTCGAGGAGCCAGCTCCCTGAGGTGGAGGAGATGCCAGAC 660
QY	661 ATGGGTGTGGGACAGTCAGCCGGTGGACAGCTGGCCTGTGACTGTGTCCTCAAGAA 720
Db	661 ATGGGTGTGGGACAGTCAGCCGGTGGACAGCTGGCCTGTGACTGTGTCCTCAAGAA 720
QY	721 GACTACGAGAACTAAAGAGCACGGACGGCTCAGGGAGGTGCTGAGCAGCAGG 780
Db	721 GACTACGAGAACTAAAGAGCACGGACGGCTCAGGGAGGTGCTGAGCAGCAGG 780
QY	781 AAGGATTGTTTCTCTCAGAACAGCAAGTGTGAGACAGTCTACTCTGAATATGATAGGGC 840
Db	781 AAGGATTGTTTCTCTCAGAACAGCAAGTGTGAGACAGTCTACTCTGAATATGATAGGGC 840
QY	841 AAGTTAGACTGAGTCAGTCAGCCAGAACCTACAGTGTGACAGGAATCATGAGC 900
Db	841 AAGTTAGACTGAGTCAGTCAGCCAGAACCTACAGTGTGACAGGAATCATGAGC 900
QY	901 CTGAAAGAGCTAAGGAGCTGCTGAGGAACACTGACCTGACACAGTGGCAGTGTGAG 960
Db	901 CTGAAAGAGCTAAGGAGCTGCTGAGGAACACTGACCTGACACAGTGGCAGTGTGAG 960
QY	961 ACTGTCGACCGCCTGGTTAGAGAGGCCAGCCAGCCAGCAGTGGAGGTGAATCTGAGCTCCG 1020
Db	961 ACTGTCGACCGCCTGGTTAGAGAGGCCAGCCAGCCAGCAGTGGAGGTGAATCTGAGCTCCG 1020
QY	1021 CGGCCATCTTCGGTATGATGATTGACTCATGTCACCTTGATGTTGAGTGTGACTTCGCCA 1080
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QY	1081 GCGGCCCTCCAGCTCCAGATGGCCAGATGGTTACTACAGAAAACCTTGGCTTAGAGAAGTCACAC 1140
Db	1081 GCGGCCCTCCAGCTCCAGATGGCCAGATGGCTTAGAGAAGTCACAC 1140
QY	1141 TCCCAATTCAAGGATGTCCTCCAGAAGATATGCAAGGCCAGAGGAGTCCAGTC 1200
Db	1141 TCCCAATTCAAGGATGTCCTCCAGAAGATATGCAAGGCCAGAGGAGTCCAGTC 1200
QY	1201 TCACTGGTGGCCAGAGCTGTCAGGAGGAGCCAGATGAGRAACTGTTGGTGGCTTCCT 1260
Db	1201 TCACTGGTGGCCAGAGCTGTCAGGAGGAGCCAGATGAGRAACTGTTGGTGGCTTCCT 1260
QY	1261 ATTTGTCGGATGCCATCTAGGCCAGAAGACAGCCAAAGGCCAGAGTCCAGTCAGTCC 1320
Db	1261 ATTTGTCGGATGCCATCTAGGCCAGAAGACAGCCAAAGGCCAGAGTCCAGTCAGTCC 1320
QY	1321 TCTTGAGCAGAAAGATGTGGTAGAGCAGGAGCTGATGGGCTGGTGGCCAGACAAATTG 1380
Db	1321 TCTTGAGCAGAAAGATGTGGTAGAGCAGGAGCTGATGGGCTGGTGGCCAGACAAATTG 1380
QY	1381 ATCCAGCCTACTGACAGCTGATGTCGGCCATGCTGCTTAAGCCAGACAGT 1440
Db	1381 ATCCAGCCTACTGACAGCTGATGTCGGCCATGCTGCTTAAGCCAGACAGT 1440
QY	1441 AAGCAGGGTAGGGTAGAGCAGCCCTCTCTCTCCAGGCCAGCTGACACTTC 1500
Db	1441 AAGCAGGGTAGGGTAGAGCAGCCCTCTCTCCAGGCCAGCTGACACTTC 1500
QY	1501 CTGGGTGTGAGAACAGTGTGAGCTGACCTGCTGAGGAGCTGACACTGTGAG 1560
Db	1501 CTGGGTGTGAGAACAGTGTGAGCTGACCTGCTGAGGAGCTGACACTGTGAG 1560
QY	1561 TCAAGGACTGTCAGCCAGSSTTGTGAGAAGAGGCCACTGGGACGCCAGCTGAGGT 1620
Db	1561 TCAAGGACTGTCAGCCAGSSTTGTGAGAAGAGGCCACTGGGACGCCAGCTGAGGT 1620
QY	1621 GTAGGGAGAACAGGAGGTGAGGTGAGCTGACCTGCTGAGCAGACTGTGCTTCTGCT 1680
Db	1621 GTAGGGAGAACAGGAGGTGAGCTGACCTGCTGAGCAGACTGTGCTTCTGCT 1680
QY	1681 CACCTGGCCCACTCTACGAGCTGAGCAGCCACTGATCTGTGTCAGCA 1740
Db	1681 CACCTGGCCCACTCTACGAGCTGAGCAGCCACTGATCTGTGTCAGCA 1740
QY	1741 GGTCTCTCTGTTGCCAGGCTCTGTTAGCCATGATGATGAGTGTGGTCAGACTCTT 1800



QY	796	TCCGAAAGCAGAATGCAAGACAGCTACTCGTAATTGGATAGGCCAAGTTAGAAGCTGAG	840
Db	781	TCCGAAGCAAGTGCAGACAGTCTACTCGTAATTGGATAGGCCAAGTTAGAAGCTGAG	855
QY	856	TCAGCCCAGAAGGACTTACAGAGTGTGAGAATGAGAAATCTGAGGCTGAAAGAGCTA	915
Db	841	TCAGCCCAAGAAGGACTTACAGAGTGTGAGAATGAGAAATCTGAGGCTGAAAGAGCTA	900
QY	916	AGGATGCTGAGGAAACCTGACCTGAGCCACAGTGGCCAGTGTGAGACTGTCACCTGAG	975
Db	901	AGGATGCTGAGGAAACCTGACCTGAGCCACAGTGGCCAGTGTGAGACTGTCACCTGAG	960
QY	976	GTTTAGAGAAGCCAGCCCCCTGGAGGTGATATCGAAGTGCAGGGGACATCTTCCT	1035
Db	961	GTTTAGAGAAGCCAGCCCCCTGGAGGTGATATCGAAGTGCAGGGGACATCTTCCT	1020
Db	1021	GATGATATTGATCTCATGCTACCTTGATGATGAGTACTCCCAAGCCCCGCCCCCTCCAG	1095
QY	1036	GATGATATTGATCTCATGCTACCTTGATGATGAGTACTCCCAAGCCCCGCCCCCTCCAG	1111
Db	1111	GATGATATTGATCTCATGCTACCTTGATGATGAGTACTCCCAAGCCCCGCCCCCTCCAG	1080
QY	1096	TCCGACCATGCTTACTACGAAACCTTGCTAGAGACTGACACTCCCCAATTCAGGAT	1155
Db	1081	TCCGACCATGCTTACTACGAAACCTTGCTAGAGACTGACACTCCCCAATTCAGGAT	1140
QY	1156	GTCCCCAAGAAGATATCGAAGGCCAGGAGGACTCCAGCTCATGGTGGATCCAG	1215
Db	1141	GTCCCCAAGAAGATATCGAAGGCCAGGAGGACTCCAGCTCATGGTGGATCCAG	1200
QY	1216	AGCTGTCAGGAGAGCCAGATGAGGACTGTTGGTGCCTTCCTATTGTGCGGAT	1275
Db	1201	AGCTGTCAGGAGAGCCAGATGAGGACTGTTGGTGCCTTCCTATTGTGCGGAT	1260
QY	1276	GCCATCCTAGGCCAGAACGCCAAAAGGCCAACAGTCAGACTCTCTGCAGGAAGAT	1335
Db	1261	GCCATCCTAGGCCAGAACAGGCCAACAGGCCAACAGGCCAACAGTCAAGTCTCTGAGA	1320
QY	1336	GTGGTAGGAGCAGGCTCTGATGGCTCGGTCGCGGACAAATTATCGACGCCACTGAC	1395
Db	1321	GTGGTAGGAGCAGGCTCTGATGGCTCGGTCGCGGACAAATTATCGACGCCACTGAC	1380
QY	1396	ACAGTCATGATCCGCCATTGCTGTAAACCCAGACCAAGGTTAAGCAGGGTGAG	1455
Db	1381	ACAGTCATGATCCGCCATTGCTGTAAACCCAGACCAAGGTTAAGCAGGGTGAG	1440
QY	1456	GTGAAGACGCCGCTCTCTCTCCAGGCCAGCGGACACTCTCTGGCTGTGAGAA	1515
Db	1441	GTGAAGACGCCGCTCTCTCTCCAGGCCAGCGGACACTCTCTGGCTGTGAGAA	1500
QY	1516	CAGTGTCTGCCAACATGGCGACACATCCTGACTGTGAGTCAGGACTGTCCAG	1575
Db	1501	CAGTGTCTGCCAACATGGCGACACATCCTGACTGTGAGTCAGGACTGTCCAG	1560
QY	1576	GCAGGG--TGTGGACAGGCCCTACTTGGGACCGCCGACTTGGGACCCAGCTGAGGTGAGGGCAGACA	1633
Db	1561	GCAGGGTTGTGGACAGGCCCTACTTGGGACCCAGCTGAGGTGAGGGCAGACA	1620
QY	1634	AACAGTGTGGAGTGTGACACCCAGACACTGCTCTCTGCGCTCACCTGCCAC	1693
Db	1621	AACAGTGTGGAGTGTGACACCCAGACACTGCTCTCTGCGCTCACCTGCCAC	1680
QY	1694	TCTTACGACCTGGGACTGATGACATGACCCACTGCTGGACCCACTGCTGGCTCTCT -CTG	1752
Db	1681	TCTTACGACCTGGGACTGATGACATGACCCACTGCTGGACCCACTGCTGGCTCTCT	1740
QY	1753	TGGCAGGCTCTGTGTTATGCCATGATCGATGCTGGGAGACTCTTGTGAGCTGAG	1812
Db	1741	TGGCAGGCTCTGTGTTATGCCATGATCGATGCTGGGAGACTCTTGTGAGCTGAG	1800
QY	1813	ACCACGGTCACTGTGACTGCTCTGAGGCTCAGGCCACCTGCTGGCTCTCTGAG	1872
Db	1801	ACCACGGTCACTGTGACTGCTCTGAGGCTCAGGCCACCTGCTGGCTCTCTGAG	1860
QY	1873	TGAGCCAAAGTCTACCTGCTTGTGACTGCTCTA -GCAAGCTCTGGGCCAGCAGG	1931

RESULT	3
LOCUS	BC000310
DEFINITION	Homo sapiens, TRAF interacting protein, clone MGC:8424
IMAGE	2821007, mRNA, complete cds.
ACCESSION	BC000310
VERSION	BC000310.1
KEYWORDS	MGC.
ORGANISM	human.
HOME sapiens	
REFERENCE	BC000310
AUTHORS	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo; Homo; 1 (bases 1 to 2010)
JOURNAL	Strasbourg, R.
COMMENT	Direct Submission
REMARK	Submitted (15 NOV 2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NCI-MGC Project URL:	<a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a>
Contact:	MGC help desk
Email:	<a href="mailto:cgabps@mail.nih.gov">cgabps@mail.nih.gov</a>
Tissue procurement:	DCTD/DTP
CDNA Library Preparation:	Rubin laboratory
CDNA Library Arrayed by:	The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by:	National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland;
Web site:	<a href="http://www.nisc.nih.gov/">http://www.nisc.nih.gov/</a>
Contact:	<a href="mailto:nisc-mocenbgri.nih.gov">nisc-mocenbgri.nih.gov</a>
Shevchenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.N., Brinkley, C., Brooks, S., Dierrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karins, E., Legaspi, R., Lim, M., Maduro, O.L., Masilio, C., Mastrian, S.D., McCloskey, J.C., McDowell, J.J., Pearson, R., Snyder, B., Santripop, S., Thomas, P.J., Tiengson, E.E., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Zhang, L.-H. and Green, E.D.	
Clone distribution:	MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a>
Series:	IRAL Plate: 1 Row: e Column: 7
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 5032194.	

BASE COUNT	ORIGIN	517 a	519 c	561 g	413 t	413 t	
Query	Match	94.2%	Score	1891.2	DB	9	
Best	Local Similarity	98.4%	Pred.	No. 0	Mismatches	23	
Matches	1964	Conservative	0	Indels	9	Gaps	5
Oy	20	GAAGCAAGGGAGGCGCGGC--	CTCTAGAAGSCGGACCTGAGCTGAGCTTCTTGGC	75	Db	10	
Db	10	GAGCAAGGGAGGCGGGGGCGCTACGAAGGGACCTGTAGCAGT	69	Qy	976		
Oy	76	TGCCCTGGGCCCTGTAGTCCAGCACATGCTATCGTGTCTGCGACTATCGCTCC	135	Db	970		
Db	70	TGCCCTGGGCCCTGTAGTCCAGCACATGCTATCGTGTCTGCGACTATCGCTCC	129	Qy	1036		
Oy	136	GACTCTCTGACTCCCGCACGTOGCCACATCCACTGGGCCACACCTTCACTG	195	Db	1030		
Db	130	GACTTCCTCGATCAGTCCGGACGCGGCCATTCACITCGGCCACACTTCCACTG	189	Qy	1096		
Oy	196	CACTGCTTAATTCAGTCTTNGAGACAGCACCAAGTGGACCTGCCCACATC	255	Db	1090		
Db	190	CACTGCTTAATTCAGTGTGAGACAGCACCAAGTGGACCTGCCACAGTGGCAATC	249	Qy	1156		
Oy	256	CAGGTGGCAAAAGAACATPATCAATAAGCTTCTTGTCTGCCAGGAGGAG	315	Db	1150		
Db	250	CAGGTGGCAAAAGAACATPATCAATAAGCTTCTTGTCTGCCAGGAGGAG	309	Qy	1216		
Oy	316	AATGCTCTGGATGGAGATTCCTTAAGATGAGTGGACAATGTCAGAGCCACGCTTCC	375	Db	1210		
Db	310	AATGCTCTGGATGGAGATTCCTTAAGATGAGTGGACAATGTCAGAGCCACGCTTCC	369	Qy	1276		
Oy	376	CAGAAAGAACAGGAGAACAGCACAGCCAGTGTAGCGAGCAGGCCAGTACGCTG	435	Db	1270		
Db	370	CAGAAAGAACAGGAGAACAGCACAGCCAGTGTAGCGAGCAGGCCAGTACGCTG	429	Qy	1336		
Oy	436	GRAGAACGCAATGCTACTGCTGATCCTGAGCAGGCCAGTGGCAGGGAGGCTG	495	Db	1330		
Db	430	GRAGAACGCAATGCTACTGCTGATCCTGAGCAGGCCAGTGGCAGGGAGGAG	489	Qy	1396		
Oy	496	TGCTCCACACTGAAAGCAGATGAGTACTTGAGCAGCAGCAGGATGAGACAA	555	Db	1450		
Db	490	TGCTCCACACTGAAAGCAGATGAGTACTTGAGCAGCAGCAGGATGAGACAA	549	Qy	1516		
Oy	556	GCACAAAGGGGGGGGGGGCTCAGAGCAAGATGGAGCACATGGAGCATGTAGCT	615	Db	1510		
Db	550	GCACAAAGGGGGGGGGGGCTCAGAGCAAGATGGAGCATGTAGCT	609	Qy	1576		
Oy	616	CTACTCCAGAGCCAGTCCCTGAGGGAGGAGATCCAGACATGGGGTGGCAG	675	Db	1630		
Db	610	CTACTCCAGAGCCAGTCCCTGAGGGAGGAGATCCAGACATGGGGTGGCAG	669	Qy	1694		
Oy	676	TCAGCGTGGACAGCTGGCTGTACTCTGCTCTCAGAAGAGTAGAGAATCTA	735	Db	1690		
Db	670	TCAGCGTGGACAGCTGGCTGTACTCTGCTCTCAGAAGAGTAGAGAATCTA	729	Qy	1634		
Oy	736	AAAGAGGCCACGGAGGCCCTCAGGGAGGATTTGTGTTCC	795	Db	1753		
Db	730	AAAGAGGCCACGGAGGCCCTCAGGGAGGATTTGTGTTCC	789	Qy	1750		
Oy	796	TCCAGAGCAAGTGTAGACAGCTACTCTGCTCTCAGAAGAGTAGAGCTGAG	855	Db	1813		
Db	790	TCCAGAGCAAGTGTAGACAGCTACTCTGCTCTCAGAAGAGTAGAGCTGAG	849	Qy	1873		
Oy	856	TCAGCCAGAGGACTACAGATGCTGACAGAAATCATGAGCTGAAAGAGCTA	915	Db	1870		
Db	850	TCAGCCAGAGGACTACAGATGCTGACAGAAATCATGAGCTGAAAGAGCTA	909	Qy	1932		

QY	1992	AAAAAAAAAAAAA	2007
Db	1989	AAATTAAAAAAA	2004
RESULT	4		
AR072729	AR072729	2065 bp	DNA
LOCUS	Sequence 1	from patent	PAT 28-AUG-2000
DEFINITION	Modulators of BRC1 activity	US 5948643.	linear
ACCESSION	AR072729	Patent: US 5948643-A	PAT
VERSION	AR072729.1	1. 07-SEP-1999	28
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 2065)		
AUTHORS	Rubinfeld, B., Polakis, P.G., Lingenfelter, C. and Vuong, T.T.		
TITLE	Modulators of BRC1 activity		
JOURNAL			
FEATURES			
source	Location/Qualifiers		
BASE COUNT	561 a	/organism="unknown"	1. 2065
ORIGIN	526 c	561 g	417 t
Query Match	94.2%	Score 1890.8;	DB 6; Length 2065;
Best Local Similarity	98.9%	DB 6; Pred. No. 0;	Length 2065;
Matches	1946; Conservative	DB 6; Mismatches 0;	Indels 5; Gaps 4;
QY	44	TACGAAGCCGGACCTGTAGCAGCTTCTTGGCTGCCCTGAGTCAGCCATCA	103
Db	44	TACGAAGCCGGACCTGTAGCAGCTTCTTGGCTGCCCTGAGTCAGCCATCA	103
QY	104	TGCTCTATGCCGCTCTCTGCACTATCGCTCGACTCTCTGTTGATCAGTCGAGTGTG	163
Db	104	TGCTCTATGCCGCTCTCTGCACTATCGCTCGACTCTCTGTTGATCAGTCGAGTGTG	163
QY	164	CGCGCCTTCACTCGGCCAACACTCCACTTCAGTCAGCTTCTGAGCCATCA	223
Db	164	CGCGCCTTCACTCGGCCAACACTCCACTTCAGTCAGCTTCTGAGCCATCA	223
QY	224	CACCAACTCGGACCTGTGCCAACAGTCAGGTGGTGCACAAAGACCAATTATA	283
Db	224	CACCAACTCGGACCTGTGCCAACAGTCAGGTGGTGCACAAAGACCAATTATA	283
QY	284	AGCTCTCTGTATGATCTGCCAGGAGAACTCTGTGATCAGATCTAAAGA	343
Db	284	AGCTCTCTGTATGATCTGCCAGGAGAACTCTGTGATCAGATCTAAAGA	343
QY	344	ATGAACTGGACATCTCAGGCCACGTTCCAGAAAGACAGAGAGACGCC	403
Db	344	ATGAACTGGACATCTCAGGCCACGTTCCAGAAAGACAGAGAGACGCC	403
QY	404	AGGTCTCATGGACACTCTGGGGATACGGCTGGAAAGACCAATGTCTC	463
Db	404	AGGTCTCATGGACACTCTGGGGATACGGCTGGAAAGACCAATGTCTC	463
QY	464	TCCAGAGCCCTGGCAAGCCGATGCTGTCACACTGAAACACGAGTA	523
Db	464	TCCAGAGCCCTGGCAAGCCGATGCTGTCACACTGAAACACGAGTA	523
QY	524	ACTTAGAGCCAGGAGATGGTGGAAAGTCAGCGGCTGCTGAGCT	583
Db	524	ACTTAGAGCCAGGAGATGGTGGAAAGTCAGCGGCTGCTGAGCT	583
QY	584	GCAAGATGAGACCATGAGCAGATGAGCTCTACCTCCAGGACGCC	643
Db	584	GCAAGATGAGACCATGAGCAGATGAGCTCTACCTCCAGGACGCC	643
QY	644	AGGAGATGAGCCAGGACATGGTGGAAAGTCAGCGGCTGCTGAGCT	703
Db	644	AGGAGATGAGCCAGGACATGGTGGAAAGTCAGCGGCTGCTGAGCT	703

Qy	1781	CAGATGTTGTCAGACTTTCGGGCTGGAGAACGGTCACTTGTGACTGTCCTGT	1840	Qy	284	AGCTCTTCTGATCTTGCCCCAGGAGGAATGTCCTGATCGAAATCTTAAGA	343
Db	1784	CAGATGTTGTCAGACTTTCGGGCTGGAGAACGGTCACTTGTGACTGTCCTGT	1843	Db	284	AGCTCTTCTGATCTTGCCCCAGGAGGAATGTCCTGATCGAAATCTTAAGA	343
Qy	1841	GGACCAAGAGTGTGCTGAGGATCTCAGGCAGGCTCAGCCAAAGCTCTACCTGCTTGAC	1900	Qy	344	ATGAACTGGACATGTCAGASGCCACGGTCTCCAGAAGAGAACGGAGACGCC	403
Db	1844	GGACCAAGAGTGTGCTGAGGATCTCAGGCAGGCTCAGCCAAAGCTCTACCTGCTTGAC	1903	Db	344	ATGAACTGGACATGTCAGASGCCACGGTCTCCAGAAGAGAACGGAGACGCC	403
Qy	1901	TTCCTCTA-GCATGCGCTGGCCAAACGAGGGTGGGAATGGAGATGAGATGGATGT	1959	Qy	404	AGTCATCATCGACACTCTGGGATACGCTGAGAAGAACGGATGCTACGGTAC	463
Db	1904	TTCCTCTA-GCATGCGCTGGCCAAACGAGGGTGGGAATGGAGATGAGATGGATGT	1962	Db	404	AGTCATCATCGACACTCTGGGATACGCTGAGAAGAACGGATGCTACGGTAC	463
Qy	1960	ATGAGAGGATGAAAGTTCCGAAAGAAAAAAAGAAAAAA 2007		Qy	464	TGGAGCAGGCCCTGGGAGGGCAGATGCTGCTGCTCCACAGGAAACGCAATGCTG	523
Db	1963	ATGAGAGGATGAAAGTTCCGAAAGAAAAAAAGAAAAAA 2010		Db	464	TGGAGCAGGCCCTGGGAGGGCAGATGCTGCTGCTCCACAGGAAACGCAATGCTG	523
RESULT	5			Qy	524	ACTTAGAGCAGCAGGATGAGACCAACAGCACAGAACAGAGGAGGGGGCGCTCGGA	583
LOCUS	BD056990		2065 bp	DNA	linear	PAT 31-JAN-2002	
DEFINITION	Modulators of BRCAl activity.			Db	524	ACTTAGAGCAGCAGGATGAGACCAACAGCACAGAACAGAGGAGGGGCCGCTCGGA	583
ACCESSION	BD056990			Db	584	GCAGAGTGAAGACATGGGAGATGAGCTTACCTCCAGGAGCAGCTCCAGGAG	643
VERSION	BD056990.1			Db	584	GCAGAGTGAAGACATGGGAGATGAGCTTACCTCCAGGAGCAGCTCCAGGAG	643
KEYWORDS	JP 20150893-A/1.			Qy	644	AGGAGATGATCCGAGACATGGGTGGGACAGTCAGGGTGGACAGCTGGGTGTACT	703
SOURCE	unclassified			Db	644	AGGAGATGATCCGAGACATGGGTGGGACAGTCAGGGTGGACAGCTGGGTGTACT	703
REFERENCE	1 (bases 1 to 2065)			Qy	704	GTGTGTCCTCAGAAGAGTAGAGATCTAAAGGGACGGAGGACCTCAGGGAGG	763
AUTHORS	Lubinfeld, B., Porakisu, P., Rigenferuta, C. and Buon, T.T.			Db	704	GTGTGTCCTCAGAAGAGTAGAGATCTAAAGGGACGGAGGACCTCAGGGAGG	763
TITLE	Modulators of BRCAl activity			Qy	764	TGGCTGACACGTGAGGATTCAGGAGCTAACGATGCTACTCCAGAGGAGCAGTACT	823
JOURNAL	Patent: JP 201502893-A 1 06-MAR-2001;			Db	764	TGGCTGACACGTGAGGATTCAGGAGCTAACGATGCTACTCCAGAGGAGCAGTACT	823
COMMENT	ONIX PHARMACEUTICALS INC			Qy	884	ACAGGAATCATGAGGCTGAAAGAGRAAGCTAACGATGCTGAGGAGCTGAGCTG	943
OS	Unidentified			Db	884	ACAGGAATCATGAGGCTGAAAGAGRAAGCTAACGATGCTGAGGAGCTGAGCTG	943
PN	JP 201502893-A/1			Qy	944	CACCACTGGGAGTGGAGACTGCGACGCCCTGCTGTGTTAGAGGCCAGCCTGTGAGG	1003
PD	06-MAR-2001			Db	944	CACCACTGGGAGTGGAGACTGCGACGCCCTGCTGTGTTAGAGGCCAGCCTGTGAGG	1003
PF	06-AUG-1997 JP 199812659			Qy	1004	TGATCTGAGCTCGCGGCATCCCTCGTGTGATGATGCTCAATGTCATCTTG	1063
PR	04-SEP-1996 US 60/025601			Db	1004	TGATCTGAGCTCGCGGCATCCCTCGTGTGATGATGCTCAATGTCATCTTG	1063
PT	BONY LUBINFEILD, PAUL PORAKISU, CAROL RIGENFERUTA, TERIRIN T BUON			Qy	1064	ATGTTGAACTCCGCCGCGCCCTCCAGCTCCGATGATGATGCTCAATGTCATCTTG	1123
PC	C12N15/09, A61K38/00, A61P43/00, C07K14/435, C07R16/18, C12N1/15,			Db	1064	ATGTTGAACTCCGCCGCGCCCTCCAGCTCCGATGATGATGCTCAATGTCATCTTG	1123
PC	C12N15/19, C12N1/21, C12N5/10, C12P21/02, C12P21/08, C12N15/00, C12N5/00, PC			Qy	1124	GCCTAGAGTCCACACTCCCAATTCAGGAGTCCAGGAGATATGCAAGGCCAA	1183
PC	A61K37/02			Db	1124	GCCTAGAGTCCACACTCCCAATTCAGGAGTCCAGGAGATATGCAAGGCCAA	1183
CC	Strandedness: Double;			Qy	1184	GGAGGAGTCCACACTCCCAATTCAGGAGTCCAGGAGATATGCAAGGCCAA	1243
CC	Topology: Linear;			Db	1184	GGAGGAGTCCACACTCCCAATTCAGGAGTCCAGGAGATATGCAAGGCCAA	1243
FH	Key			Qy	1244	TGGTGGCCCTCCCTATTGTCGGGAATGCCATCTCCAGGAGATATGCAAGGCCAA	1303
FT	CDS			Db	1244	TGGTGGCCCTCCCTATTGTCGGGAATGCCATCTCCAGGAGATATGCAAGGCCAA	1303
FEATURES	Location/Qualifiers			Qy	1304	GCCTAGAGTCCACACTCCCAATTCAGGAGTCCAGGAGATATGCAAGGCCAA	1363
SOURCE	1. . 2065			Db	1304	GCCTAGAGTCCACACTCCCAATTCAGGAGTCCAGGAGATATGCAAGGCCAA	1363
BASE COUNT	561 a 526 c 561 g 417 t						
ORIGIN							
Query Match	94.2%	Score 1890.8;	DB 6;	length 2065;			
Best Local Similarity	98.9%	Pred. No. 0;	Mismatches 17;	Indels 5;	Gaps 4;		
Matches 1946;	Conservative						
Qy	44	TTGCAAGCCGACCTGTAGCACTTCTTGGTGCCTGGCCCTTGAGTCAGCCATCA	103				
Db	44	TAGGAAGCCGACCTGTAGCACTTCTTGGTGCCTGGCCCTTGAGTCAGCCATCA	103				
Qy	104	TGGCTATCGTGCCTGTGACACTATGCTCGGACTCTTCGATCACTCCTCCGGACCTGG	163				
Db	104	TGGCTATCGTGCCTGTGACACTATGCTCGGACTCTTCGATCACTCCTCCGGACCTGG	163				
Qy	164	CGCCCATCCACTCGGCGCACACTCTCCACTTGCTGAGGAGCTTGAGTCAGGAG	223				
Db	164	CGCCCATCCACTCGGCGCACACTCTCCACTTGCTGAGGAGCTTGAGTCAGGAG	223				
Qy	224	CAACCAAGTGGGACTCTGCCACAGTGGCAATCCAGGTGGCAAAAGACCATTTATCATA	283				
Db	224	CAACCAAGTGGGACTCTGCCACAGTGGCAATCCAGGTGGCAAAAGACCATTTATCATA	283				

FEATURES	Source	passed the following selection criteria: matched mRNA 91: 6755868.
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		/tissue_type="Mammary tumor metastasized to lung. Tumor
		arose spontaneously from a <i>severe</i> normal mammary
		(clonal) outgrowth infected with the virus MMTV."
		/clone_id="MCL_CGAP_Lu29"
		/lab_host="DH10B"
		/note="Vector: pCMV-SPOR6"
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		CKMKMPEOELLIOSORSEVEEMIRDMGVSOSAVPOLAVYCVSILKE
		GELADRLKDLVILIVVLLQDNLKQDNLKQDNLKQDNLKQDNLKQDNL
		TLSPDPATNPENIVSPLVYFESPAVEMPNPQDNLVNTDVTPTQSQ
		HCLPRLKLRRARSMDMONVKKVHVSKPSOLSFGGQDVGELDEELA
		AVLGOKQPNNTTAAESRCSTDVNRIGFDGLGRTKFIQPRTTITRVPV
		VSKASKSKQ
		BASE COUNT
		582 a 489 c 528 g 425 t
		ORIGIN
		Query Match
		54.28%; Score 1087; DB 10; Length 2024;
		Best Local Similarity 74.9%; Pred. No. 3; 4e-23;
		Matches 1492; Conservative 0; Mismatches 440; Indels 61; Gaps 8;
		QY 26 AGCGGAGGGGGCGCTCTAGAACGGGACCTGTAGCAGTTCTCTGGCGCC 85
		Db 26 AGCGGAGGGGGCGCTCTAGAACGGGACCTGTAGCAGTTCTCTGGCGCC 84
		QY 86 CCTTCTAGTCAGCCATCATGCCTATCGTGTCTGACTATCGTCTCGACTCTTG 145
		Db 85 CCTTCTAGTCAGCCATCATGCCTATCGTGTCTGACTATCGTCTCGACTCTTG 144
		QY 146 ATCACCTCCGGGACCTGGCCGCCACCCACTCGGGCACACCTCCACTTGCTGCTAA 205
		Db 145 ATCACCTCCGGGACCTGCATGCCTATCGGCGCTCTGACTATCGTCTCGACTCTTG 204
		QY 206 TTCACTCTTGAGCACAGCACCAACTGGGACCTGGCCACACTGCGCAATCAGGTGGCA 265
		Db 205 TCCASTGTTGAGAGCACCAACTGGGACCTGGCCACACTGCGCAATCAGGTGGCA 264
		QY 266 AAAGAACCTATCATCAAACTTCTTGTGCTGGCCAGGAGGAGAATGCTTGG 325
		Db 265 AAAGAACCTATCATCAAACTTCTTGTGCTGGCCAGGAGGAGAATGCTTGG 324
		QY 326 ATCGAATTCTAAGAATGACCGACAATGTCAGGCCAGCTTCCAGAAGACA 385
		Db 325 ATCGAATTCTAAGAATGACCGACAATGTCAGGCCAGCTTCCAGAAGACA 384
		QY 386 AGGAGAACGAGACGCCAGCTCATCGACACTCTGCGGACATCGCTGAGAACGCA 445
		Db 385 GGAGAACGAGACGCCAGCTCATCGACACTCTGCGGACACCTGGAGAACGCA 444
		QY 446 ATGCTACTCTGAGGACTCTGAGGCCAGCTTGGGAGGGAGATGCTGCTCACAC 505
		Db 445 ATGCTACTCTGAGGACTCTGAGGCCAGCTTGGGAGGGAGATGCTGCTCACAC 504
		Anup Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
		Clone distribution: MGC clone distribution information can be found
		through the T.M.A.G.E. Consortium/LINL at: <a href="http://image.lnl.gov">http://image.lnl.gov</a>
		Series: IRAK Plate: 18 Row: d Column: 5
		This clone was selected for full length sequencing because it
		passed the following selection criteria: matched mRNA 91: 6755868.
		Location/Qualifiers
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		/ab_xref="LocusID:22036"
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		arose spontaneously from a <i>severe</i> normal mammary
		(clonal) outgrowth infected with the virus MMTV."
		/clone_id="MCL_CGAP_Lu29"
		/lab_host="DH10B"
		/note="Vector: pCMV-SPOR6"
		102..1514
		/codon_start=1
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		CKMKMPEOELLIOSORSEVEEMIRDMGVSOSAVPOLAVYCVSILKE
		GELADRLKDLVILIVVLLQDNLKQDNLKQDNLKQDNLKQDNLKQDNL
		TLSPDPATNPENIVSPLVYFESPAVEMPNPQDNLVNTDVTPTQSQ
		HCLPRLKLRRARSMDMONVKKVHVSKPSOLSFGGQDVGELDEELA
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		BASE COUNT
		582 a 489 c 528 g 425 t
		ORIGIN
		Query Match
		54.28%; Score 1087; DB 10; Length 2024;
		Best Local Similarity 74.9%; Pred. No. 3; 4e-23;
		Matches 1492; Conservative 0; Mismatches 440; Indels 61; Gaps 8;
		QY 26 AGCGGAGGGGGCGCTCTAGAACGGGACCTGTAGCAGTTCTCTGGCGCC 85
		Db 26 AGCGGAGGGGGCGCTCTAGAACGGGACCTGTAGCAGTTCTCTGGCGCC 84
		QY 86 CCTTCTAGTCAGCCATCATGCCTATCGTGTCTGACTATCGTCTCGACTCTTG 145
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		QY 146 ATCACCTCCGGGACCTGGCCGCCACCCACTCGGGCACACCTCCACTTGCTGCTAA 205
		Db 145 ATCACCTCCGGGACCTGCATGCCTATCGGCGCTCTGACTATCGTCTCGACTCTTG 204
		QY 206 TTCACTCTTGAGCACAGCACCAACTGGGACCTGGCCACACTGCGCAATCAGGTGGCA 265
		Db 205 TCCASTGTTGAGAGCACCAACTGGGACCTGGCCACACTGCGCAATCAGGTGGCA 264
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		Db 385 GGAGAACGAGACGCCAGCTCATCGACACTCTGCGGACACCTGGAGAACGCA 444
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		Anup Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
		Clone distribution: MGC clone distribution information can be found
		through the T.M.A.G.E. Consortium/LINL at: <a href="http://image.lnl.gov">http://image.lnl.gov</a>
		Series: IRAK Plate: 18 Row: d Column: 5
		This clone was selected for full length sequencing because it
		passed the following selection criteria: matched mRNA 91: 6755868.
		Location/Qualifiers
		1. 2024
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		/ab_xref="LocusID:22036"
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		arose spontaneously from a <i>severe</i> normal mammary
		(clonal) outgrowth infected with the virus MMTV."
		/clone_id="MCL_CGAP_Lu29"
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		/note="Vector: pCMV-SPOR6"
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		ORIGIN
		Query Match
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		Best Local Similarity 74.9%; Pred. No. 3; 4e-23;
		Matches 1492; Conservative 0; Mismatches 440; Indels 61; Gaps 8;
		QY 26 AGCGGAGGGGGCGCTCTAGAACGGGACCTGTAGCAGTTCTCTGGCGCC 85
		Db 26 AGCGGAGGGGGCGCTCTAGAACGGGACCTGTAGCAGTTCTCTGGCGCC 84
		QY 86 CCTTCTAGTCAGCCATCATGCCTATCGTGTCTGACTATCGTCTCGACTCTTG 145
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		QY 146 ATCACCTCCGGGACCTGGCCGCCACCCACTCGGGCACACCTCCACTTGCTGCTAA 205
		Db 145 ATCACCTCCGGGACCTGCATGCCTATCGGCGCTCTGACTATCGTCTCGACTCTTG 204
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		Db 205 TCCASTGTTGAGAGCACCAACTGGGACCTGGCCACACTGCGCAATCAGGTGGCA 264
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		Db 325 ATCGAATTCTAAGAATGACCGACAATGTCAGGCCAGCTTCCAGAAGACA 384
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		Anup Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
		Clone distribution: MGC clone distribution information can be found
		through the T.M.A.G.E. Consortium/LINL at: <a href="http://image.lnl.gov">http://image.lnl.gov</a>
		Series: IRAK Plate: 18 Row: d Column: 5
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		arose spontaneously from a <i>severe</i> normal mammary
		(clonal) outgrowth infected with the virus MMTV."
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		TITDURDLBTERNATIVESLONALNRAEMLVCNUFLQDKRQDLSQ
		CKMKMPEOELLIOSORSEVEEMIRDMGVSOSAVPOLAVYCVSILKE
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		QY 26 AGCGGAGGGGGCGCTCTAGAACGGGACCTGTAGCAGTTCTCTGGCGCC 85
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		Anup Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
		Clone distribution: MGC clone distribution information can be found
		through the T.M.A.G.E. Consortium/LINL at: <a href="http://image.lnl.gov">http://image.lnl.gov</a>
		Series: IRAK Plate: 18 Row: d Column: 5
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		passed the following selection criteria: matched mRNA 91: 6755868.
		Location/Qualifiers
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		/ab_xref="taxon:10000"
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		/tissue_type="Mammary tumor metastasized to lung. Tumor
		arose spontaneously from a <i>severe</i> normal mammary
		(clonal) outgrowth infected with the virus MMTV."
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		582 a 489 c 528 g 425 t
		ORIGIN
		Query Match
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		Best Local Similarity 74.9%; Pred. No. 3; 4e-23;
		Matches 1492; Conservative 0; Mismatches 440; Indels 61; Gaps 8;
		QY 26 AGCGGAGGGGGCGCTCTAGAACGGGACCTGTAGCAGTTCTCTGGCGCC 85
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		QY 86 CCTTCTAGTCAGCCATCATGCCTATCGTGTCTGACTATCGTCTCGACTCTTG 145
		Db 85 CCTTCTAGTCAGCCATCATGCCTATCGGCGCTCTGACTATCGTCTCGACTCTTG 144
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</		



BASE COUNT		532 a	489 c	534 g	426 t
ORIGIN					
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Db	15	GTGCGGGGAGGCCAAATTGAGAACGCCAGGGGGGGG - GCTCTACGAGGCCGACCT 74			
Qy	59	GTAGCACTTCTTGCTGCTGGGCCCTTGAGTCCAGGCATCATGCCATCGCTATCGCT 118			
Db	75	GTCTCTG - GCGCTGTTCTGGGGCTTGAGTCCAGGCATCATGCCATCGCTATCGCT 133			
Qy	119	TGTGCACTATCTGCTCGACTCTTCGATCACTCCCGCAGGTGGCGCATTCACTGCG 178			
Db	134	TGTGCACTATCTGCTCGACTCTTCGATCACTCCCGTGAAGCTGGCTGCCAGCTGCG 193			
Qy	179	GCCACACCTTCACATGCAAGGCTTAATCGTCTTGAGACAGCAGCTGGACCT 238			
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Qy	239	GCCACAGTGCAGTCAGGTTGCCAAAGAACCAATTATCAATAGCTCTCTTGATC 298			
Db	254	GCCACAGTGTAGAACGCCAGTTGGCCAAAGAACATTATAAACAACTTTCTTGAC 313			
Qy	299	TTGCCAGGAGGAGGAGAATGATCTCTTGATGAGAACTCTAAGAATGAACTGGACATG 358			
Db	314	TCGCCAGGAGGAGGAGAATGCTTGGATGAGAACTCTAAGAATGAACTGGACAGCG 373			
Qy	359	TCGAGGCCAGCTTCCAGAACAGAACAGAACAGAACAGAACAGCTGGATCAG 418			
Db	374	TCAAACTCTACCTTCCAGAAGAACAGGGAGAACGGAGAACAGCCAGTGGACAG 433			
Qy	419	CTCTGGGATACTGGAGAACGCAATGCTACTCTGGATCTCTGAGCAGGGCTGG 478			
Db	434	CTCTAGGGACACCCGTGGAAGAACCAAATGCTACGGGGACTCTACAGAACGCTAA 493			
Qy	479	GCAAGCCAGATGCTGCTGCCACACTGAAACAGATGAGAACTTAGAGCAGCAG 538			
Db	494	ACAAGCCAGATGCTGCTCCACCTGAAAACAGATGAGTCTCTGGAGAACGGCG 553			
Qy	539	AGGAGGAGAACAAAGAACAGAACAGAACAGAACAGAACAGAACAGAACAG 593			
Db	554	AGGATGAGAACACAGCTGGAGGAGGCCACGGCACTGAGAACAGAACAGAAC 613			
Qy	599	TGGAGCAGATGAGCTCTACTCCAGAGGCCAGCTCTGGTGGAGGATGATCGAG 658			
Db	614	TGGAGCAATTGAGCCTACTCTCAGAGGCCAGCTCTGGTGGAGGATGATCGAG 673			
Qy	659	ACATGGGTGGAGACGTGCGGGCTAGAGGCCAGCTGGCTGGTGGAGGAGGAG 718			
Db	674	ACATGGGTGGAGACGTGCGGGCTAGAGGCCAGCTGGCTGGTGGAGGAGGAGGAG 733			
Qy	719	AAGACTTACGAGAACATAAGAGGCCAGGGAGGCTCAGGGAGGGCTGGCTGGAG 778			
Db	734	AAGAGTATGAGAACATCGAGGAGACCTGGGAGGCCACAGGGAGACTGGCTGG 793			
Qy	779	GGAGGATGCTTCTCCAGAGCAAGTGGCAGACAGCTCTGAATTGGATCAGG 838			
Db	794	AGAAGGATGTTGGCTCTCAGGAGCAAGTGGAGACTCTCAAACTGAGCTGGATCAGG 853			
Qy	839	CCAGTGTAGACTGAGTCAGGCCAGAACAGTACAGAGTGTGCAAGAGAAATCATGA 898			
Db	854	CCAACTAGACTGAGTCAGGCCAGAACAGTACAAAGTGTGCAACCAGGAGTCAGGA 913			
Qy	899	GCCGAAAGAAGCTAACCGATGCTGCCAGGAACCTGACCTGCCACAGTGGCCAGTC 958			
Db	914	GCCTAAAGAAAGCAGTATCCCTCCAGGGAACCTTGACCTGCTCCCGTACCAATG 973			
Qy	959	AGACTCTGACGCCCTGGTTAGAGAGGCCAGGCCCTGGGA -- GGTGAACTGAGC 1015			
Db	974	AGACGTCACGCCGCTGGTTTGAGGCCAGGCCCTGGAGATGAGAACCGAGGCC 1033			
Qy	1016	TCCGGGGCCATCCCTCGGATGATTATCTCAATGCTACCTTGTAGTGGTGTAC 1075			
Db	1034	CTCCAAAGCCAGACCTCTGGCCTCCAGCATTCCTCCAAAGAACGCTGTGTAATACCC 1093			
Qy	1076	CCCAACCCGCCCCCTCCAGGCTGGCTGGAGTACTACGAAAACCTTGCCTAGAAGC 1135			
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Qy	1136	CAACATCCCAATTGAGATGCTCCCAAGAGAGATGAGAAGGGCCAGGCCCTGGTCC 1195			
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Qy	1196	AGCTCTACCTGGTGGCAGACGCTGAGCTGAGAGAACCCAGTGGTGGTGTGCT 1255			
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Qy	1256	TCCCTATTGTCGCGAAGTGGCATCTAGCCAGAACGAGGAGTCCAAAGAAGCT 1315			
Db	1274	TCCCTCTCTCATCGGAGATGCTGCTGTGCTGGTCAAGAGGTCACAGGAGCTGG 1333			
Qy	1316	AGTCCTCTSCAGGAAGTGTGGAGGAGCAGCTGGTCAAGGAGGACAGGCCAGAC 1375			
Db	1334	AATCCGAAAGCAGAACGAGAACGAGAACGAGAACGGCCAGTCAGGCCAGTCAG 1393			
Qy	1376	ATTCTATCCAGCTACTGAGACAGTCATGTCGCCATTGCGCTTAAGGCCAGACA 1435			
Db	1394	AATTCATCCAGCTAGGAGACACACTTTCGACCAAGCCAGGCCACAGGACAGCAG 1453			
Qy	1436	AGGTAAAGCAGGGTTGGAGGAGACGCTGGTAAAGAAGCTGAGTGTGCTGGATA 1495			
Db	1454	AGAGTAAACGAGAACTGAGATAAAGAAGCTGAGTGTGAGTGTGCTGGATA 1513			
Qy	1496	CCTCTCTGTCGAGACACAGTCAGTGTGCTGGCTCCCTCTCAGGCCAGTCAC 1555			
Db	1514	AGGTAAAGCAGGGTTGGAGGAGACGAGTGGTGGAGGAGCTGGTGGAGGAGACA 1558			
Qy	1556	GTAGGTCAAGGACTGTCCA - GGCAAGGTTGTGGACAGAGCCCTACTTCGGACACC 1613			
Db	1559	GTGGCCAAAGACCTGCTAACCGGAGTGTGGAGGAGTGTGGAGGAGTGGCTCC 1614			
Qy	1614	CTGAGGTGTAGGGAGACACAGGTGGAGGTGAGTGTGACACCCAGAGACTCTC 1673			
Db	1615	-----AGTCCAGAGAGGATGCCAGAACACACTC 1646			
Qy	1674	CTGCCCTACCTGCCCCACTCTACAGCTGGGAGCTGAGATGCCAGCCACAGTCAT 1733			
Db	1647	CTGTGTTCTACAGCCGCTGACCTGACCTGAGTGTGCTGGAGCTGGTGTGACCG 1704			
Qy	1734	GTCAAGGCTCTGC - TCTGTGCAAGGCTCTGGTTATAGCCATGATCAGATGGTCA 1792			
Db	1705	ATCACGAGCCCTACTTCGGTGTGGGTTCTGAGTGTGCTGACACGGGCTGGCT 1764			
Qy	1793	GACTCTCTGGGCTGGAGACACAGGTGACTCTGTTGAGTGTGCTGTGAGGACCG 1847			
Db	1765	GACTCTCTGGGCTGGAGACACAGGTGACTCTGTTGAGTGTGCTGTGAGGACCG 1884			
Qy	1848	AGTGTGTTGAGCAGTCAGCCAGCTGAGCTGAGTGTGCTGTGAGTGTGCT 1907			
Db	1885	TGAAATTGGGGTGGAGGAGTGGGAAGTGGGAAGTGGGAGTGGGAGTGGTGTGTA 1944			
Qy	1968	GATGAAAGATTTCCGAAAAAAGCTAACCGATGCTGCCAGGAACCTGACCTGCCAGTC 2004			

RESULT	8
BC006929	BC006929 3694 bp mRNA linear ROD 12-JUL-2001
LOCUS	Mus musculus, TRAF-interacting protein, clone MGC:11463
DEFINITION	Mus musculus, TRAF-interacting protein, clone MGC:11463
ACCESSION	IMAGE:315502, mRNA, complete cds.
VERSION	BC006929
KEYWORDS	MGC.
ORGANISM	Mus musculus
COMMENT	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 3694)
REFERENCE	Strausberg, R.
AUTHORS	Direct Submission
TITLE	Submitted (27-APR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK	NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a>
COMMENT	Email: cgabbs-r@mail.nih.gov
TISSUE	Procurement: Jeffrey Green M.D.
CDNA LIBRARY	Preparation: Life Technologies, Inc.
CDNA LIBRARY	Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA	Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
Center code: BCM-HGSC	
Web site: <a href="http://www.hgsc.bcm.tmc.edu/cdna/">http://www.hgsc.bcm.tmc.edu/cdna/</a>	
VILLALON	Contact: villalon@bcm.tmc.edu
D.K., LUNA, R.A., HALE, S.M., HILYK, S., LU, X., GARCIA, A.M., HOLLOWAY, M., TELFORD, B., HODGSON, A., BOUCK, J., YU, W., MUZNY, D.M., GIBBS, R.A.	
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a>	
Series: IRAK plate: 16 Row: a Column: 23	
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 2039305. Location/Qualifiers	
FEATURES	
source	
1. .3694	
/organism="Mus musculus"	
/ab_xref="LocusID:22036"	
/ab_xref="taxon_id:10090"	
/clone="MGC:11463 IMAGE:315502"	
/tissue_type="Mammary tumor, C3(1)-Tag model. Infiltrating ductal carcinoma. 5 month old virgin mouse."	
/clone_id="NCI_CGAP_Mam6"	
/lab_host="BIRI0B"	
/note="Vector: pENV-SPORT6"	
CDS	
277. .948	
/codon_start=1	
/product="TRAF-interacting protein"	
/protein_id="AAH0929_1"	
/ab_xref="GI:13905262"	
/translation="MPTIALCTCSDFDHSRWAATHGHTHLQCLIOWFETAPSRTPOCRQVKFLINKFLDIAQEEVNLDAEFLKNEFLSKVQLSKDRKRSQFLIDTLRDLERNAVTEQLQNAFLKMLCSTKQDDETKDQAREEAKRLCWNKTMBSQELLIQSQSPREVEEMTRDMQVQGOSAVEQLAVYCVSLKKCVSSGVPLPSSFWQIL"	
BASE COUNT	858 a 951 c 976 g 909 t
ORIGIN	
Query Match	26 0%; Score 521 6; DB 10; Length 3694;
Best Local Similarity	81.8%; Pred. No. 1.1e-134;
Matches	569; Conservative 0; Mismatches 79; Indels 0; Gaps 0;
Y	72 TGGCTGCTGGGCCCTTGAAGTCAGCCATCATGCCTATCCGGTCTCTGCACTATCTG 131
RESULT	9
HS465N24	HS465N24 129747 bp DNA linear PRI 23-NOV-1999
LOCUS	Human DNA sequence from clone 465N24 on chromosome 1p35.1-36.13.
DEFINITION	Contains two novel genes, ESTs, GSSs and Cpg islands, complete sequence.
ACCESSION	AL031432
VERSION	AL031432.1 GI:4175969
KEYWORDS	HTG; Cpg Island.
SOURCE	human.
ORGANISM	Homo sapiens
COMMENT	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 129747)
REFERENCE	Wilson, S.
AUTHORS	Direct Submission
TITLE	Submitted (11-FEB-1999) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
JOURNAL	On Mar 7, 1999 this sequence version replaced gi:4176479. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence is the entire insert of clone 465N24. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known

annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/chr1>. 465N24 is from the library RIC13 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see <http://bacpac.med.buffalo.edu/> VECTOR: pcYPAC2. Location/Qualifiers

FEATURES	SOURCE
repeat_region	1. 129747 'organism' "Homo sapiens" 'db_xref' "taxon:9606" 'chromosome' "1" 'map' "p35.1-36.13" 'clone' "RJ3-465N24" 'clone_id' "RP01-3" 540..753 2061..2268 975..1303 'note' "AluJo repeat: matches 1..311 of consensus" repeat_region 2356..2518 'note' "MER5A repeat: matches 5..164 of consensus" repeat_region 2519..2827 'note' "MIR repeat: matches 29..262 of consensus" repeat_region 3245..3360 'note' "MIR repeat: matches 100..262 of consensus" repeat_region 3427..3485 'note' "L2 repeat: matches 2688..2746 of consensus" repeat_region 3444..3676 'note' "AluYb8 repeat: matches 1..318 of consensus" repeat_region 3690..3856 'note' "L1R41 repeat: matches 20..139 of consensus" repeat_region 4187..4494 'note' "AluSg repeat: matches 1..308 of consensus" repeat_region 4846..5143 'note' "MIR repeat: matches 8..249 of consensus" repeat_region 5287..5340 'note' "L1MD1 repeat: matches 5345..5398 of consensus" repeat_region 5361..5518 'note' "L1MA4 repeat: matches 6152..6300 of consensus" repeat_region 5508..6164 'note' "L1MD1 repeat: matches 5423..6091 of consensus" repeat_region 6176..6245 'note' "35 copies 2 mer ta 73% conserved" repeat_region 6247..6288 'note' "AluSg repeat: matches 15..291 of consensus" repeat_region 6529..6674 'note' "73 copies 2 mer ta 73% conserved" repeat_region 6741..6874 'note' "L1MD1 repeat: matches 6090..6223 of consensus" repeat_region 7225..7278 'note' "MIR repeat: matches 36..85 of consensus" repeat_region 8137..8448 'note' "AluSx repeat: matches 1..312 of consensus" repeat_region 9092..9137 'note' "23 copies 2 mer at 100% conserved" repeat_region 9229..9226 'note' "L2 repeat: matches 2574..2670 of consensus" repeat_region 9669..9732 'note' "MIR repeat: matches 87..148 of consensus" repeat_region 10162..10365 'note' "MIR repeat: matches 8..222 of consensus" repeat_region 10359..10505 'note' "L2 repeat: matches 2586..2710 of consensus" repeat_region 10654..10814 'note' "MER86 repeat: matches 9..176 of consensus" repeat_region 11454..11752 'note' "MER86 repeat: matches 4928..5368 of consensus"
repeat_region	/note="AluJb repeat: matches 1..302 of consensus" 11790..12171 /note="L1M4 repeat: matches 1258..1640 of consensus" repeat_region 12172..12362 /note="MER3 repeat: matches 1..189 of consensus" repeat_region 12363..12775 /note="L1M4 repeat: matches 1640..2049 of consensus" repeat_region 12833..13130 /note="AluJo repeat: matches 1..291 of consensus" repeat_region 13476..14035 /note="L1M4 repeat: matches 2224..2742 of consensus" repeat_region 14036..14330 /note="AluY repeat: matches 1..301 of consensus" repeat_region 14331..14466 /note="L1M4 repeat: matches 2742..2867 of consensus" repeat_region 14467..14600 /note="FLAMC repeat: matches 1..133 of consensus" repeat_region 14601..14885 /note="L1M4 repeat: matches 2867..3278 of consensus" repeat_region 14893..15096 /note="L1M4 repeat: matches 286..505 of consensus" repeat_region 15159..15484 /note="L1MD repeat: matches 6..323 of consensus" repeat_region 15487..16041 /note="L1M4 repeat: matches 7451..7973 of consensus" repeat_region 16069..16773 /note="L1MB3A repeat: matches 286..3943 of consensus" repeat_region 16774..17068 /note="AluSg repeat: matches 3..297 of consensus" repeat_region 17071..17384 /note="L1M4 repeat: matches 1..310 of consensus" repeat_region 17385..17451 /note="L1MB3A repeat: matches 3943..3955 of consensus" repeat_region 17567..17775 /note="L1MB3A repeat: matches 4012..4208 of consensus" repeat_region 17912..18219 /note="AluSg repeat: matches 1..313 of consensus" repeat_region 18401..18922 /note="L1MB3A repeat: matches 4315..4848 of consensus" repeat_region 18923..19226 /note="AluSx repeat: matches 1..304 of consensus" repeat_region 19227..19530 /note="L1MB3A repeat: matches 4848..4886 of consensus" repeat_region 19531..19897 /note="L1PB1 repeat: matches 5781..6155 of consensus" repeat_region 19898..20698 /note="L1MB3A repeat: matches 4585..5403 of consensus" repeat_region 21061..21150 /note="MIR repeat: matches 115..213 of consensus" repeat_region 21218..21390 /note="L2 repeat: matches 1626..1814 of consensus" repeat_region 21511..21767 /note="L1MC2 repeat: matches 6664..6940 of consensus" repeat_region 21771..21969 /note="L1MC2 repeat: matches 3850..4054 of consensus" repeat_region 21970..22008 /note="U2 repeat: matches 1..39 of consensus" repeat_region 22009..22354 /note="L1MC2 repeat: matches 4054..4410 of consensus" repeat_region 22355..22663 /note="L1MC2 repeat: matches 1..309 of consensus" repeat_region 22664..23540 /note="L1MC2 repeat: matches 4410..5261 of consensus" repeat_region 23552..23730 /note="L1MC2 repeat: matches 4054..4410 of consensus" repeat_region 23731..24657 /note="AluSx repeat: matches 1..5278..6319 of consensus" repeat_region 24659..24758 /note="AluJ/FLAM repeat: matches 2..77 of consensus" repeat_region 24759..25029 /note="L1MB5 repeat: matches 7461..7777 of consensus" repeat_region 25872..26333 /note="L1MB5 repeat: matches 4928..5368 of consensus"

repeat_region	26334 .. 26622	Db	25540 CCTGGAGACAGAGTCATTGTGACTGTCTCTATGGACCAAGCTTGGAGGCATCTCA 25599
repeat_region	/note="L1MB8 repeat: matches 5995. .6287 of consensus"	Qy	1866 GGCAGCTCTGCCAAGCTCTACCTGGCTTGACTGTCTCA GCATGCCCTGGCCA 1924
repeat_region	/note="L1MB5 repeat: matches 5368. .5512 of consensus"	Db	25600 GGCAGACTAACTGAGTTCTACCTCTGCTGACTGTCTAGGCCATGCTGGCCA 25659
repeat_region	/note="L1MB5 repeat: matches 5512. .6176 of consensus"	Qy	1925 ACCGGGTGGAAATGGAGATAGCATGGATGTTGGAGAGGATTTCCCG 1984
repeat_region	/note="ALuY repeat: matches 74. .299 of consensus"	Db	25660 AGCAGGGTGGAAATGGAGAT-----GGAGGTGGAGGAGATAATTTCATG 25712
repeat_region	/note="L1MC3 repeat: matches 6941. .7003 of consensus"	Qy	1985 AAAAAAAA..... 2004
repeat_region	/note="tandem repeat in single clone region"	Db	25713 TAAACTTTAAAGAA 25732
repeat_region	/note="L2 repeat: matches 2241. .2422 of consensus"	Db	25732 TAAACTTTAAAGAA 25732
repeat_region	29643 .. 30184	Qy	1866 GGCAGCTCTGCCAAGCTCTACCTGGCTTGACTGTCTCA GCATGCCCTGGCCA 1924
repeat_region	/note="LTR22 repeat: matches 1. .505 of consensus"	Db	25600 GGCAGACTAACTGAGTTCTACCTCTGCTGACTGTCTAGGCCATGCTGGCCA 25659
repeat_region	/note="MIR repeat: matches 28. .118 of consensus"	Qy	1925 ACCGGGTGGAAATGGAGATAGCATGGATGTTGGAGAGGATTTCCCG 1984
repeat_region	/note="L2 repeat: matches 1794. .1967 of consensus"	Db	25660 AGCAGGGTGGAAATGGAGAT-----GGAGGTGGAGGAGATAATTTCATG 25712
repeat_region	/note="MIR repeat: matches 187. .261 of consensus"	Qy	1985 AAAAAAAA..... 2004
repeat_region	31416 .. 31494	Db	25713 TAAACTTTAAAGAA 25732
repeat_region	/note="MIR repeat: matches 2241. .2422 of consensus"	Db	25732 TAAACTTTAAAGAA 25732
Query Match	13.0%; Score 260; DB 9; Length 129747;	RESULT	10
Best Local Similarity	68.4%; Pred. No. 3..6e-61; Matches 547; Conservative	LOCUS	G23637/c
Matches 547; Conservative	0; Mismatches 140; Indels 113; Gaps 9;	DEFINITION	human STS WI-13434, sequence tagged site.
		ACCESSION	G23637
		REFERENCE	G23637.1 GI:1343963
		AUTHORS	1 (bases 1 to 391)
		TITLE	Hudson, T.
		ORGANISM	Whitehead Institute/MIT Center for Genome Research; Physically
		COMMENT	mapped STS
		CONTACT	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
		REFERENCE	Whitehead Institute/MIT Center for Genome Research
		KEYWORDS	STS; STS sequence; primer; sequence tagged site.
		SOURCE	human STSs derived from sequences in dbEST and the UniGene collection.
		ORGANISM	Homo sapiens
		COMMENT	Unpublished
		CONTACT	Thomas Hudson
		REFERENCE	Whitehead Institute/MIT Center for Genome Research
		KEYWORDS	9 Cambridge Center, Cambridge MA 02142 USA
		SOURCE	Tel: 617 252 1900
		ORGANISM	Fax: 617 252 1902
		COMMENT	Email: thudson@genome.wi.mit.edu
		CONTACT	Primer A: TACAGTAAATCTTCATCCATCTCT
		REFERENCE	Primer B: CTGUGGACCAAGAGTGCTTGA
		KEYWORDS	STS size: 150
		SOURCE	PCR profile:
		ORGANISM	Prerelease:
		COMMENT	Denaturation:
		CONTACT	Annealing: 56 degrees C
		REFERENCE	Polymerization:
		KEYWORDS	PCR Cycles: 35
		SOURCE	Thermal Cycler:
		ORGANISM	Protocol:
		COMMENT	Template: 10 ng
		REFERENCE	Primer: each 5 pm
		KEYWORDS	dNTPs: each 4 nM
		SOURCE	Taq Polymerase: 0.025 units/ul
		ORGANISM	Total Vol: 20 ul
		COMMENT	Buffer:
		REFERENCE	MgCl2: 1.5 mM
		KEYWORDS	KCl: 50 mM
		SOURCE	Tris-HCl: 10 mM
		ORGANISM	pH: 9.3
		COMMENT	Derived from dbEST (genbank accession R40580).
		REFERENCE	Location/Qualifiers
		KEYWORDS	1. .391
		SOURCE	/organism="Homo sapiens"
		ORGANISM	/db_xref="taxon:9606"
		COMMENT	/map="198.8.cR from top of chr3 linkage group"
		ORGANISM	32. .181
		COMMENT	32. .55
		ORGANISM	primer_bind complement(162. .181)



FEATURES \* 119478 163424: contig of 43947 bp in length.  
 Location/Qualifiers  
 source 1. 163424  
 /organism="Homo sapiens"  
 /db\_xref="taxon: 9606"  
 /clone="RPI1-78010"  
 /clone\_id="RPCI human BAC library 11"  
 1. 4608  
 /note="assembly\_name:Contig74"  
 4709. 10289  
 /note="assembly\_name:Contig75"  
 1030. 17105  
 /note="assembly\_name:Contig77"  
 45201. 45100  
 /note="assembly\_name:Contig78"  
 17205. 65174  
 /note="assembly\_name:Contig79"  
 90820. 119377  
 /note="assembly\_name:Contig80"  
 119478. 163424  
 /note="assembly\_name:Contig81"  
 40950 a 40937 C 39779 g 40912 t 846 others  
 BASE COUNT ORIGIN

Query Match 8.8%; Score 176.4; DB 2; Length 163424;  
 Best Local Similarity 95.1%; Pred. No. 9\_9e-38;  
 Matches 194; Conservative 0; Mismatches 6; Indels 4; Gaps 1;  
 QY 1 GAGCGGGGAGGAAATTGAAAGCAAGGGAGGGGGCG---CCTACAAAGCGGAC 56  
 Db 149275 GCTGCTGGGAGGCAAATTGAGAACGAAAGGGAGGGGGGGCGTACAGCGAC 149334  
 Qy 57 CTGTAGCAGTTCTTGCTGCTGGGCCCTGAGTCACCCATCATGCTATCGTGC 116  
 Db 149335 CTGTAGCAGTTCTTGCTGCTGGGCCCTGAGTCACCCATATCGCTATCGTGC 149394  
 Qy 117 TCTGTGACTATCTGCTCCGACTCTCGATGACTCCCGCGAGGTGCCGCATCCACTG 176  
 Db 149395 TCTGTGACTATCTGCTCCGACTCTCGATGACTCCCGCGAGGTGCCGCATCCACTG 149454  
 Qy 177 CGGCCACACCTCTACACTTGAGTG 200  
 Db 149455 CGGCCACACCTCTACACTTGAGTG 149478

RESULT 13  
 AL353694\_2/c  
 WPCOMMENT  
 Sequence split into 4 fragments LOCUS AL353694 Accession AL353694  
 Fragment Name Begin End  
 AL353694\_0 1 110000  
 AL353694\_1 100001 210000  
 AL353694\_2 200001 310000  
 AL353694\_3 300001 356330  
 Continuation (3 of 4) of AL353694 from base 200001 (AL353694 Homo sapiens chromosome 6 c

Query Match 6.5%; Score 130; DB 2; Length 110000;  
 Best Local Similarity 100.0%; Pred. No. 9\_4e-25;  
 Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 381 AGCAAGAGAACGAGACAGGCCAGGTCATCGACACTCTGGGATACCTGGAGA 440  
 Db 62746 AGCAAGAGAACGAGACAGGCCAGGTCATCGACACTCTGGGATACCTGGAGA 62687  
 Qy 441 AGCGAATGCTACTGTGTTATCTGCAAGCAGGCCCTGGCAAGGCCAGAGCTCTGGCTC 500  
 Db 62686 AGCGAATGCTACTGTGTTATCTGCAAGCAGGCCCTGGCAAGGCCAGAGCTCTGGCTC 62627

RESULT 14  
 AC099330/c AC099330  
 LOCUS AC099330 163424 bp DNA linear HTG 09-NOV-2001  
 DEFINITION Homo sapiens chromosome 3 clone RPI1-78010, WORKING DRAFT SEQUENCE,  
 8 unordered pieces.  
 AC099330 AC060701  
 AC099330\_1 GT:16374864  
 HTG; HTGS\_PHASE1; HTGS\_DRAFT; HTGS\_FULLTOP; HTGS\_ACTIVEFIN  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 163424)  
 AUTHORS Kauj, R., Olson, M. V., Raymond, C. and Haugen, E. D.  
 TITLE Direct Submission  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 163424)  
 AUTHORS Kauj, R. K., Olson, M. V., Raymond, C. and Haugen, E. D.  
 TITLE Direct Submission  
 JOURNAL Submitted (09-NOV-2001) Genome Center, University of Washington,  
 Box 352145, Seattle, WA 98195, USA  
 On Nov 9, 2001 this sequence version replaced g1:8247914.  
 COMMENT  
 Center: University of Washington Genome Center  
 Center Code: UWGC  
 Web site: <http://www.genome.washington.edu>  
 Contact: uwgc@igs.ewu.washington.edu  
 ----- Project Information  
 Center project name: chr-3  
 Center clone name: RPI1-78010 (bc0618)  
 ----- Summary Statistics  
 Sequencing vector: Unknown; 42% of reads  
 Sequencing vector: Plasmid; 58% of reads  
 Chemistry: Dye-terminator ET; 92% of reads  
 Chemistry: Dye-terminator Big Dye; 8% of reads  
 Assembly program: Phrap; version 0.990319  
 Consensus quality: 158959 bases at least 040  
 Consensus quality: 160979 bases at least 030  
 Consensus quality: 162023 bases at least 020  
 Insert size: 202900; 21.9% error; agarose-fp  
 Insert size: 162724; sum-of-contigs  
 Quality coverage: 9.0x in 020 bases; agarose-fp  
 Quality coverage: 11.2x in Q20 bases; sum-of-contigs  
 -----  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 8 contigs. The true order of the pieces is  
 \* not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.  
 \* 1 4608: contig of 4608 bp in length  
 \* \* 4609 4708: gap of unknown length  
 \* \* 4709 10289: contig of 5581 bp in length  
 \* \* 10290 10389: gap of unknown length  
 \* \* 10390 17105: contig of 6716 bp in length  
 \* \* 17105 17205: gap of unknown length  
 \* \* 17206 45100: contig of 27895 bp in length  
 \* \* 45101 45200: gap of unknown length  
 \* \* 45201 65174: contig of 19974 bp in length  
 \* \* 65175 65274: gap of unknown length  
 \* \* 65275 90720: contig of 25415 bp in length  
 \* \* 90720 90819: gap of unknown length  
 \* \* 90820 119377: contig of 28558 bp in length  
 \* \* 119378 119477: gap of unknown length  
 \* 119478 163424: contig of 43947 bp in length.







RESULT	18	143948	152393: contig of 8446 bp in length
REFERENCE	AC073495/C	152394	152393: gap of unknown length
LOCUS	AC073495	152494	152494: contig of 7933 bp in length
DEFINITION	MUS musculus chromosome 11 clone RP23-345K4, WORKING DRAFT	160427	160426: gap of unknown length
ACCESSION	AC073495	160527	160543: contig of 6117 bp in length
VERSION	AC073495.12	166644	166743: gap of unknown length
KEYWORDS	GI:10801940	166744	166743: contig of 6117 bp in length
SOURCE	HGSC_PHASE1; HTGS_DRAFT.	173855	173855: gap of 3824 bp in length
ORGANISM	house mouse.	177409	177508: gap of unknown length
Mus musculus		177509	183310: contig of 5802 bp in length
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		183311	183410: gap of unknown length
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		183411	183877: contig of 5567 bp in length
1 (bases 1 to 318930)		183878	189077: gap of unknown length
Metzker, M.L., Lewin, B.R., Hume, J., Edwards, C., Harris, C.,		189078	196629: contig of 7552 bp in length
Daderich, D., Thomas, S., Okwunuo, G., Carlock, C., Garner, T.,		196630	196729: gap of unknown length
Adolison, S., Pace, A., Williams, G., Bonin, D., Brooks, A., Brown, J.,		196730	202134: contig of 5405 bp in length
Buhay, C., Bunac, C., Burkett, C., Chacko, J., Chen, Z.,		202135	202134: gap of unknown length
Cox, C., Davis, C., Delgado, O., Ding, Y., Duan-Rocha, S.,		202335	206563: contig of 4729 bp in length
Fernandez, C., Ferraguto, D., Forcum-Tansey, J., Gill, R.,		205964	207063: gap of unknown length
Gorelli, J.H., Guarante, P., Haller, G., Hernandez, J., Hogues, M.,		207064	212314: contig of 5251 bp in length
Hesak, H., Hou, X., Huber, J., Jackson, L., Jia, Y., Kelly, J., Kelly, S.,		212315	212141: gap of unknown length
Kovar, C., Liu, J., Liu, W., Louisberg, H., Lozado, R.J., Martin, R.,		212415	216415: contig of 4001 bp in length
Massey, E., McLeod, M.P., Mei, G., Moore, S., Morgan, M., Morris, S.,		216416	219635: gap of 3110 bp in length
Neal, D., Nelson, A., Nguyen, R., Nguyen, N., Oguh, M., Parish, B.,		216626	219626: gap of unknown length
Perez, L., Reiter, D., Say, J., Shen, H., Vasquez, L., Watlington, S.,		219726	224004: contig of 4279 bp in length
Williamson, A., Wrenfrod, G., Zhou, X., Bouck, J., Hodgson, A.,		224005	224104: gap of unknown length
Muzny, D.M., Rives, M., Scherer, S., Sodergren, E., Weinstock, G.,		224105	227363: contig of 3259 bp in length
Worley, K. and Gibbs, R.		227364	227363: gap of unknown length
Direct Submission	Unpublished	227464	232010: contig of 4547 bp in length
REFERENCE	2 (bases 1 to 318930)	232011	232110: gap of unknown length
AUTHORS	Worley, K.C.	232111	234956: contig of 2845 bp in length
TITLE	Direct Submission	234956	235055: gap of unknown length
JOURNAL		235056	238628: contig of 3573 bp in length
COMMENT	Submitted (19-JUN-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA	238729	242373: contig of 3645 bp in length
On Oct 15, 2000 this sequence version replaced 91:10800205.		242374	242473: gap of unknown length
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Center: Baylor College of Medicine		244475	244574: gap of unknown length
Center code: BCM		244575	247650: contig of 3076 bp in length
Web site: <a href="http://www.hgsc.bcm.tmc.edu/">http://www.hgsc.bcm.tmc.edu/</a>		247651	247755: gap of unknown length
Contact: hgsc-help@bcm.tmc.edu		247751	250706: contig of 2950 bp in length
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Center project name: MACH		250807	253666: contig of 2840 bp in length
Center clone name: RP23-345K4		253677	253746: gap of unknown length
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Sequencing vector: M13; L08821		255998	255997: gap of unknown length
Chemistry: Dye-primer Bodipy; 71% of reads.		255998	258504: contig of 2507 bp in length
Chemistry: Dye-terminator Big Dye: 29% of reads.		258505	258664: gap of unknown length
Assembly program: Phrap; version 0.990329		258805	260676: contig of 2072 bp in length
Consensus quality: 282577 bases at least 040		260577	260765: gap of unknown length
Consensus quality: 299603 bases at least 030		260777	263190: contig of 2414 bp in length
Consensus quality: 309271 bases at least Q20		263190	263200: gap of unknown length
Estimated insert size: 298164; sum-of-contigs estimation		263391	264984: contig of 1694 bp in length
Quality coverage: 0x in Q20 bases; agarose-fp estimation		264985	265004: gap of unknown length
Quality coverage: 5.1x in Q20 bases; sum-of-contigs estimation		265085	266722: contig of 1638 bp in length
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NOTE: Estimated insert size may differ from sequence length		266847:	266847: contig of 1650 bp in length
(see <a href="http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html">http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html</a> )		266847:	266847: gap of unknown length
NOTE: This sequence may represent more than one clone.		26873	270376: contig of 1804 bp in length
NOTE: This is a 'working draft' sequence. It currently		270377	270476: gap of unknown length
consists of 64 contigs. The true order of the pieces		270476	272058: contig of 1582 bp in length
is not known and their order in this sequence record is		272059	272158: gap of unknown length
arbitrary. Gaps between the contigs are represented as		272159	274242: contig of 2084 bp in length
runs of N, but the exact sizes of the gaps are unknown.		274242	274343: gap of unknown length
This record will be updated with the finished sequence		274343	276852: contig of 2520 bp in length
as soon as it is available and the accession number will		276852	276852: gap of unknown length
be preserved.		276863	276863: contig of 2152 bp in length
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1 100449: contig of 100449 bp in length		279214	280875: contig of 1661 bp in length
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143848 143947: gap of unknown length		282744	282744: gap of unknown length



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QY	112981	gap of unknown length	
QY	113304	gap of 11515 bp in length	
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QY	136092	gap of unknown length	
QY	136415	contig of 7710 bp in length	
QY	136416	contig of 7710 bp in length	
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QY	152006	gap of unknown length	
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QY	159588	gap of unknown length	
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QY	167458	contig of 6299 bp in length	
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QY	173758	contig of 6299 bp in length	
QY	174082	contig of 5769 bp in length	
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QY	180175	contig of 5381 bp in length	
QY	185556	gap of unknown length	
QY	185879	contig of 5205 bp in length	
QY	191144	contig of 5205 bp in length	
QY	191145	gap of unknown length	
QY	191468	contig of 4945 bp in length	
QY	196413	gap of 4945 bp in length	
QY	196736	contig of 4523 bp in length	
QY	201259	gap of unknown length	
QY	201581	contig of 4168 bp in length	
QY	205750	gap of unknown length	
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QY	209960	gap of unknown length	
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QY	213541	gap of unknown length	
QY	213863	contig of 2328 bp in length.	
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	1. 216191: contig of 2328 bp in length.		
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ORIGIN	/clone="RP23-6087" /db_xref="taxon:10050" /organism="Mus musculus"		
FEATURES	source		
BASE COUNT	60680	a 45448 c 44115 g 58724 t 7224 others	
ORIGIN			
FEATURES	source		
BASE COUNT	351	a 684 c 303 g 727 t	
ORIGIN			



Qy	724	TACCGAGGATCTAAAGGAGCAGGAGCCCTAGGGAGGTTGCTGACAACGTGAGGAG 783	Schlossgarten 4, Institut für Klinische und Molekulare, Erlangen
Db	155474	CAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGCAG 155533	01054, Germany
Qy	784	GATTC 789	Sequence update by submitter
Qy	155534	AAGTAG 155539	On Jul 9, 2001 this sequence version replaced gi:2246464.
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VERSION	2	Gi:14627174	/organism="Human herpesvirus 8"
KEYWORDS			/db_xref="taxon:37296"
ORGANISM			/note="sequence derived from overlapping Lambda phage clones isolated from two libraries of Sau3A partially digested DNA from Kaposi's sarcoma biopsies"
REFERENCE	1	(bases 21733 to 118431)	105..959
AUTHORS	Zhong, W., Wang, H., Herndier, B. and Ganem, D.		/note="ORF K1"
TITLE	Restricted expression of Kaposi's sarcoma-associated herpesvirus (human herpesvirus 8) genes in Kaposi's sarcoma		/codon_start=1
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 93 (13), 6641-6646 (1996)		/protein_id="AAB62619_1"
MEDLINE	96270595		/db_xref="GI: 2246494"
REFERENCE	2	(bases 17424 to 17856)	/translation="MELIVVSLAVRGLLSLLOSSPNUCPGVISTPTLTCPSNTSLPTSWNDRLRLRQTQPTVDTLICNFCVGSGSRISLWITWYQPVLQTLQCGQPSNTVTCQHIVYLCPSNGNNVTVHILPQNGNETVSOTQKYNFTLNUQNTGCGYACSGNLLSRLSNRLCSARCANLIPETHTVSSTGFRFSTNRGCTLIDVLWKEAKSTNLHIVQHIVFVMTLVALIGTMCGILTIAFHCKQDSDNKTVPQLOQDYSLSLDCEDYQPVQWY"
AUTHORS	Neipel, F., Albrecht, J.C., Ensser, A., Huang, Y.Q., Li, J.J., Friedman-Kien, A.E. and Fleckenstein, B.		1127..2779
TITLE	Human herpesvirus 8 encodes a homolog of interleukin-5		/note="ORF 04, complement control protein homolog"
JOURNAL	J. Virol. 71 (1), 839-842 (1997)		/codon_id="AAB62602_1"
MEDLINE	97138401		/protein_id="AAB62602_1"
REFERENCE	3	(bases 123309 to 124082)	/db_xref="GI: 2246477"
AUTHORS	Li, M., Lee, H., Yoon, D.W., Albrecht, J.C., Fleckenstein, B., Neipel, F. and Jung, J.U.		/translation="MARTLQTLWLTWPTMVGQDNEKCSQTKLTYRQLRKNRSRGDIAVGETVEIRCRSGITKARNTATCLOGGTWSEPTATCNKSCPNFGEIQLKQVHGGQDALKYCANITISVNCNGCFLYGRREYRYCMIGASGOMAWSSPPCEKEKCHRPIKGYIQLGSLTYKHKRSGTACNGDLSLGPSTCNTEENDLRLKVLIEDDNPNSPGRUHPTPNKRPNGVWFORSYNTEPPTKPEDHTAATCONECDPQKLTPTSEFNEMTSNTTOKOLEDTKSITORTHTSITALTSAKAKONTFTNTNSDHTIASTPSQDDATPSIPSVQTYNTNAPTRPLSLHTEGSPNSNTSKATASTLHSNPKTQDQGIVYTLINKTQLPSTPNKPNQNSKSTAKPVEETKTSNPAISLTDSDAVPQPRETLLPPIFRPASKNLYKELOVIGLITAVALLTCGLTILPHYLFFR"
TITLE	Kaposi's sarcoma-associated herpesvirus encodes a functional cyclin		3194..6592
JOURNAL	J. Virol. 71 (3), 1984-1991 (1997)		/note="ORF 06, major ssDNA binding protein homolog"
MEDLINE	97184528		/codon_start=1
REFERENCE	4	(bases 122660 to 123226)	/protein_id="AAB62603_1"
AUTHORS	Thome, M., Schneider, P., Fickenscher, H., Meini, E., Neipel, F., Mattern, C., Burns, K., Bodmer, J.L., Schröter, M., Scaffidi, C., Krammer, P.H., Peter, M.E. and Tschopp, J.J.		/db_xref="GI: 2246478"
TITLE	Viral FLICE-inhibitory proteins (FLIPs) prevent apoptosis induced by death receptors		/translation="MALKPGPOTLENGGAAATPGCGYLYALTHPPIGRASLIGNGYPAKVSPLHGTPLQVWAKHKAQKIDTAVSKVLTSHKRTAHEVHNTFQPIFOGKSLKLCRSERFLEFGSTFVEQOKGTLWSFACPOLCANEILMAMIVTGFKRLYGGKSLVPSOTPSOTVPHGEHQHOKIPLDDEDGPSRQELCPYRNDISRYLHDSITFGQAOALVKDQVTSIQAQFQWHDQYKIKLWQVADQFQASCAGRDSTLWDSLVAEGLGMSLGSFEGPQDSCVEVNWYDTPFEMQETDPAKALEWHAQMLIDSLVQDCLASCMFBQDNPAVGTVSEWKMHQTMWTFMKGCFDKGATGELHIGQFLAANSVLYLTVRKAQPKQKNORDANMNSYQHQHGYLSATRIFNQGKIGVPSVSLDGSSTIQLHAAASSFSHLAQMCTQELPHKHTNQSINVWDVGTATPSOMCQDCGOCGOCPPVACINTYRMRKFPVPLSNVYRDPVYITGTYDLELGNFATPFREREEGPVNPDEAKYTWOLCONTEKLASMSISEGDAURLTIVDPSVKKYFQIDSVTEAELKINCKKNNFENRKSNSKSYHILQACWQAPQDQFVYKPLVQDLSLVTWQDCLASCMFBQDNPAVGTVSEWKMHQTMWTFMKGCFDKGATGELHIGQFLAANSVLYLTVRKAQPKQKNORDANMNSYQHQHGYLSATRIFNQGKIGVPSVSLDGSSTIQLHAAASSFSHLAQMCTQELPHKHTNQSINVWDVGTATPSOMCQDCGOCGOCPPVACINTYRMRKFPVPLSNVYRDPVYITGTYDLELGNFATPFREREEGPVNPDEAKYTWOLCONTEKLASMSISEGDAURLTIVDPSVKKYFQIDSVTEAELKINCKKNNFENRKSNSKSYHILQACWQAPQDQFVYKPLVQDLSLVTWQDCLASCMFBQDNPAVGTVSEWKMHQTMWTFMKGCFDKGATGELHIGQFLAANSVLYLTVRKAQPKQKNORDANMNSYQHQHGYLSATRIFNQGKIGVPSVSLDGSSTIQLHAAASSFSHLAQMCTQELPHKHTNQSINVWDVGTATPSOMCQDCGOCGOCPPVACINTYRMRKFPVPLSNVYRDPVYITGTYDLELGNFATPFREREEGPVNPDEAKYTWOLCONTEKLASMSISEGDAURLTIVDPSVKKYFQIDSVTEAELKINCKKNNFENRKSNSKSYHILQACWQAPQDQFVYKPLVQDLSLVTWQDCLASCMFBQDNPAVGTVSEWKMHQTMWTFMKGCFDKGATGELHIGQFLAANSVLYLTVRKAQPKQKNORDANMNSYQHQHGYLSATRIFNQGKIGVPSVSLDGSSTIQLHAAASSFSHLAQMCTQELPHKHTNQSINVWDVGTATPSOMCQDCGOCGOCPPVACINTYRMRKFPVPLSNVYRDPVYITGTYDLELGNFATPFREREEGPVNPDEAKYTWOLCONTEKLASMSISEGDAURLTIVDPSVKKYFQIDSVTEAELKINCKKNNFENRKSNSKSYHILQACWQAPQDQFVYKPLVQDLSLVTWQDCLASCMFBQDNPAVGTVSEWKMHQTMWTFMKGCFDKGATGELHIGQFLAANSVLYLTVRKAQPKQKNORDANMNSYQHQHGYLSATRIFNQGKIGVPSVSLDGSSTIQLHAAASSFSHLAQMCTQELPHKHTNQSINVWDVGTATPSOMCQDCGOCGOCPPVACINTYRMRKFPVPLSNVYRDPVYITGTYDLELGNFATPFREREEGPVNPDEAKYTWOLCONTEKLASMSISEGDAURLTIVDPSVKKYFQIDSVTEAELKINCKKNNFENRKSNSKSYHILQACWQAPQDQFVYKPLVQDLSLVTWQDCLASCMFBQDNPAVGTVSEWKMHQTMWTFMKGCFDKGATGELHIGQFLAANSVLYLTVRKAQPKQKNORDANMNSYQHQHGYLSATRIFNQGKIGVPSVSLDGSSTIQLHAAASSFSHLAQMCTQELPHKHTNQSINVWDVGTATPSOMCQDCGOCGOCPPVACINTYRMRKFPVPLSNVYRDPVYITGTYDLELGNFATPFREREEGPVNPDEAKYTWOLCONTEKLASMSISEGDAURLTIVDPSVKKYFQIDSVTEAELKINCKKNNFENRKSNSKSYHILQACWQAPQDQFVYKPLVQDLSLVTWQDCLASCMFBQDNPAVGTVSEWKMHQTMWTFMKGCFDKGATGELHIGQFLAANSVLYLTVRKAQPKQKNORDANMNSYQHQHGYLSATRIFNQGKIGVPSVSLDGSSTIQLHAAASSFSHLAQMCTQELPHKHTNQSINVWDVGTATPSOMCQDCGOCGOCPPVACINTYRMRKFPVPLSNVYRDPVYITGTYDLELGNFATPFREREEGPVNPDEAKYTWOLCONTEKLASMSISEGDAURLTIVDPSVKKYFQIDSVTEAELKINCKKNNFENRKSNSKSYHILQACWQAPQDQFVYKPLVQDLSLVTWQDCLASCMFBQDNPAVGTVSEWKMHQTMWTFMKGCFDKGATGELHIGQFLAANSVLYLTVRKAQPKQKNORDANMNSYQHQHGYLSATRIFNQGKIGVPSVSLDGSSTIQLHAAASSFSHLAQMCTQELPHKHTNQSINVWDVGTATPSOMCQDCGOCGOCPPVACINTYRMRKFPVPLSNVYRDPVYITGTYDLELGNFATPFREREEGPVNPDEAKYTWOLCONTEKLASMSISEGDAURLTIVDPSVKKYFQIDSVTEAELKINCKKNNFENRKSNSKSYHILQACWQAPQDQFVYKPLVQDLSLVTWQDCLASCMFBQDNPAVGTVSEWKMHQTMWTFMKGCFDKGATGELHIGQFLAANSVLYLTVRKAQPKQKNORDANMNSYQHQHGYLSATRIFNQGKIGVPSVSLDGSSTIQLHAAASSFSHLAQMCTQELPHKHTNQSINVWDVGTATPSOMCQDCGOCGOCPPVACINTYRMRKFPVPLSNVYRDPVYITGTYDLELGNFATPFREREEGPVNPDEAKYTWOLCONTEKLASMSISEGDAURLTIVDPSVKKYFQIDSVTEAELKINCKKNNFENRKSNSKSYHILQACWQAPQDQFVYKPLVQDLSLVTWQDCLASCMFBQDNPAVGTVSEWKMHQTMWTFMKGCFDKGATGELHIGQFLAANSVLYLTVRKAQPKQKNORDANMNSYQHQHGYLSATRIFNQGKIGVPSVSLDGSSTIQLHAAASSFSHLAQMCTQELPHKHTNQSINVWDVGTATPSOMCQDCGOCGOCPPVACINTYRMRKFPVPLSNVYRDPVYITGTYDLELGNFATPFREREEGPVNPDEAKYTWOLCONTEKLASMSISEGDAURLTIVDPSVKKYFQIDSVTEAELKINCKKNNFENRKSNSKSYHILQACWQAPQDQFVYKPLVQDLSLVTWQDCLASCMFBQDNPAVGTVSEWKMHQTMWTFMKGCFDKGATGELHIGQFLAANSVLYLTVRKAQPKQKNORDANMNSYQHQHGYLSATRIFNQGKIGVPSVSLDGSSTIQLHAAASSFSHLAQMCTQELPHKHTNQSINVWDVGTATPSOMCQDCGOCGOCPPVACINTYRMRKFPVPLSNVYRDPVYITGTYDLELGNFATPFREREEGPVNPDEAKYTWOLCONTEKLASMSISEGDAURLTIVDPSVKKYFQIDSVTEAELKINCKKNNFENRKSNSKSYHILQACWQAPQDQFVYKPLVQDLSLVTWQDCLASCMFBQDNPAVGTVSEWKMHQTMWTFMKGCFDKGATGELHIGQFLAANSVLYLTVRKAQPKQKNORDANMNSYQHQHGYLSATRIFNQGKIGVPSVSLDGSSTIQLHAAASSFSHLAQMCTQELPHKHTNQSINVWDVGTATPSOMCQDCGOCGOCPPVACINTYRMRKFPVPLSNVYRDPVYITGTYDLELGNFATPFREREEGPVNPDEAKYTWOLCONTEKLASMSISEGDAURLTIVDPSVKKYFQIDSVTEAELKINCKKNNFENRKSNSKSYHILQACWQAPQDQFVYKPLVQDLSLVTWQDCLASCMFBQDNPAVGTVSEWKMHQTMWTFMKGCFDKGATGELHIGQFLAANSVLYLTVRKAQPKQKNORDANMNSYQHQHGYLSATRIFNQGKIGVPSVSLDGSSTIQLHAAASSFSHLAQMCTQELPHKHTNQSINVWDVGTATPSOMCQDCGOCGOCPPVACINTYRMRKFPVPLSNVYRDPVYITGTYDLELGNFATPFREREEGPVNPDEAKYTWOLCONTEKLASMSISEGDAURLTIVDPSVKKYFQIDSVTEAELKINCKKNNFENRKSNSKSYHILQACWQAPQDQFVYKPLVQDLSLVTWQDCLASCMFBQDNPAVGTVSEWKMHQTMWTFMKGCFDKGATGELHIGQFLAANSVLYLTVRKAQPKQKNORDANMNSYQHQHGYLSATRIFNQGKIGVPSVSLDGSSTIQLHAAASSFSHLAQMCTQELPHKHTNQSINVWDVGTATPSOMCQDCGOCGOCPPVACINTYRMRKFPVPLSNVYRDPVYITGTYDLELGNFATPFREREEGPVNPDEAKYTWOLCONTEKLASMSISEGDAURLTIVDPSVKKYFQIDSVTEAELKINCKKNNFENRKSNSKSYHILQACWQAPQDQFVYKPLVQDLSLVTWQDCLASCMFBQDNPAVGTVSEWKMHQTMWTFMKGCFDKGATGELHIGQFLAANSVLYLTVRKAQPKQKNORDANMNSYQHQHGYLSATRIFNQGKIGVPSVSLDGSSTIQLHAAASSFSHLAQMCTQELPHKHTNQSINVWDVGTATPSOMCQDCGOCGOCPPVACINTYRMRKFPVPLSNVYRDPVYITGTYDLELGNFATPFREREEGPVNPDEAKYTWOLCONTEKLASMSISEGDAURLTIVDPSVKKYFQIDSVTEAELKINCKKNNFENRKSNSKSYHILQACWQAPQDQFVYKPLVQDLSLVTWQDCLASCM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misc_feature	complement(6153..6286)"	146147..146196	misc-feature	/note="sequence from uni-directional primer reads and dGTP
misc_feature	/note="match: STS: Em:LA1071"	19774..20547	misc-feature	/note="sequence from uni-directional primer reads and dGTP
misc_feature	/note="CPG island"	19774..20547	misc-feature	big dye terminator reads only."
misc_feature	/evidence-not-experimental	19774..20547	misc-feature	complement(151206..151660)
misc_feature	/note="match: GSS: Em:AZ837024"	21687..22022	misc-feature	/note="match: GSS: Em:AZ837024"
misc_feature	/note="match: GSS: Em:AZ791707"	24059..24666	misc-feature	/note="match: GSS: Em:AZ03512"
misc_feature	/note="match: GSS: Em:AZ03512"	complement(20917..21304)	misc-feature	/note="match: GSS: Em:AZ03512"
misc_feature	/note="match: GSS: Em:AZ2837075"	complement(26781..27451)	misc-feature	/note="match: GSS: Em:AZ2837075"
misc_feature	/note="match: GSS: Em:AZ260334"	complement(26962..27413)	misc-feature	/note="match: GSS: Em:AZ260334"
misc_feature	/note="match: GSS: Em:AZ303774"	complement(31902..31984)	misc-feature	/note="match: GSS: Em:AZ303774"
misc_feature	/note="match: GSS: Em:AZ271347"	complement(31985..40432)	misc-feature	/note="match: GSS: Em:AZ271347"
misc_feature	/note="match: GSS: Em:AZ771476"	complement(31992..40442)	misc-feature	/note="match: GSS: Em:AZ771476"
misc_feature	/note="match: GSS: Em:AZ771491"	complement(41322..44838)	misc-feature	/note="match: GSS: Em:AZ771491"
misc_feature	/note="match: GSS: Em:AZ224680"	47267..47315	misc-feature	/note="match: GSS: Em:AZ224680"
misc_feature	/note="match: GSS: Em:AZ753028"	52135	misc-feature	/note="match: GSS: Em:AZ753028"
misc_feature	/note="tandem repeat. Forced join. Gap sized to be approximately 1100bp from restriction digest data and spanning PUC clone."	62719..63094	misc-feature	/note="tandem repeat. Forced join. Gap sized to be approximately 1100bp from restriction digest data and spanning PUC clone."
misc_feature	/note="match: GSS: Em:AZ259817"	63094..63268	misc-feature	/note="match: GSS: Em:AZ259817"
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misc_feature	/note="match: GSS: Em:AZ032738"	63299..633297	misc-feature	/note="match: GSS: Em:AZ032738"
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misc_feature	/note="match: GSS: Em:AZ2288969"	64531..64626	misc-feature	/note="match: GSS: Em:AZ2288969"
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misc_feature	/note="match: GSS: Em:AZ394052"	64625..64625	misc-feature	/note="match: GSS: Em:AZ394052"
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misc_feature	/note="match: GSS: Em:AZ448471"	64625..64625	misc-feature	/note="match: GSS: Em:AZ448471"
misc_feature	/note="match: GSS: Em:AZ44470"	64625..64625	misc-feature	/note="match: GSS: Em:AZ44470"
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misc_feature	/evidence-not-experimental	64625..64625	misc-feature	/evidence-not-experimental
misc_feature	/note="match: GSS: Em:AZ041515"	64625..64625	misc-feature	/note="match: GSS: Em:AZ041515"
misc_feature	/note="match: GSS: Em:AZ28615T"	64625..64625	misc-feature	/note="match: GSS: Em:AZ28615T"
misc_feature	/note="match: GSS: Em:AZ05615"	64625..64625	misc-feature	/note="match: GSS: Em:AZ05615"
misc_feature	/note="match: GSS: Em:AZ266926"	64625..64625	misc-feature	/note="match: GSS: Em:AZ266926"
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misc_feature	/note="match: GSS: Em:AZ788648"	64625..64625	misc-feature	/note="match: GSS: Em:AZ788648"
misc_feature	/note="match: GSS: Em:AZ246254"	64625..64625	misc-feature	/note="match: GSS: Em:AZ246254"
misc_feature	127968..128455	64625..64625	misc-feature	127968..128455
misc_feature	complement(128635..128910)	64625..64625	misc-feature	complement(128635..128910)
misc_feature	complement(127255..127857)	64625..64625	misc-feature	complement(127255..127857)
misc_feature	143168..143545	64625..64625	misc-feature	143168..143545
misc_feature	/note="match: GSS: Em:AZ2246254"	64625..64625	misc-feature	/note="match: GSS: Em:AZ2246254"
RESULT	27			
AL609699				
LOCUS	AL609699	224712 bp	DNA	linear
DEFINITION	Mus musculus chromosome 4 clone RP23-331P21, *** SEQUENCING IN			
ACCESSION	AL609699			



Galagan, J., Gardyna, S., Gindele, S., Goyette, M., Graham, J., Grand-Pierre, N., Grant, G., Haggas, B., Heaford, A., Horrton, L., Howland, J.C., Ilie, I., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, R., Lamazares, R., Landers, T., Lehozky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, J., McGuirk, A., McKernan, K., McPheeetters, R., Medrano, J., Meneus, L., Mihow, T., Miranda, C., Menga, V., Morrow, J., Murthy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, T.M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thioman, N., Stojanovic, N., Subramanian, A., Talamas, J., Testayre, S., Theodore, J., Tirrell, A., Travers, M., Tricilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and Zody, M.

**TITLE** JOURNAL  
**COMMENT**

Submitted (28-MAR-2000) Whithead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

All repeats were identified using RepeatMasker: g1:819804.

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On May 10, 2001 this sequence version replaced g1:819804.

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On May 10, 2001 this sequence version replaced g1:819804.

**Center:** Whitehead Institute/ MIT Center for Genome Research  
**Center code:** WIBR  
**Web site:** <http://www-seq.wi.mit.edu>  
**Contact:** sequence\_submission@genome.wi.mit.edu  
**Direct Submission**  
**Center project name:** L9029  
**Center clone name:** 228\_G\_18  
**----- Summary Statistics**  
**sequencing vector:** M13; M77815; 90% of reads  
**Chemistry:** plasmid; n/a; 10% of reads  
**Assembly program:** phrap; version 0.960731  
**Consensus quality:** 150458 bases at least Q40  
**Consensus quality:** 162515 bases at least Q30  
**Consensus quality:** 166983 bases at least Q20  
**Insert size:** 153000; agarose-fp  
**Quality coverage:** 4.7 in 020 bases; agarose-fp  
**Quality coverage:** 4.2 in 020 b.  

\* NOTE: This is a working draft, sequence. It currently consists of 43 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

\* 13487: contig of 13487 bp in length

\* 13488 13587: gap of 100 bp

\* 13588 14626: contig of 1039 bp in length

\* 14627 14726: gap of 100 bp

\* 14727 15793: contig of 1067 bp in length

\* 15794 15833: gap of 100 bp

\* 15894 15707: contig of 1164 bp in length

\* 17058 17157: gap of 100 bp

\* 17158 18291: contig of 1134 bp in length

\* 18292 18392: gap of 100 bp

\* 18392 20046: contig of 1655 bp in length

\* 20047 20146: gap of 100 bp

\* 21387 21486: gap of 100 bp

\* 21487 22760: contig of 1274 bp in length

\* 22761 22890: gap of 100 bp

\* 22861 23953: contig of 1093 bp in length

\* 23954 24053: gap of 100 bp

\* 24054 25081: contig of 1028 bp in length

\* 25082 25181: gap of 100 bp

\* 25182 26357: contig of 1176 bp in length

\* 26358 26457: gap of 100 bp

\* 26458 27574: contig of 1117 bp in length

**FEATURES**  
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1. -174019 Location/Qualifiers  
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 /ab\_xref="taxon:9606"  
 /chromosome="15"  
 /map="15"  
 /clone="RP11-226G18"  
 /clone\_1lib="RPCI-11 Human Male BAC"  
 1..11487 misc\_feature  
 /note=assembly\_fragment  
 clone\_end:516











Query Match 2.8%; Score 55.4; DB 14; length 3127;  
 Best Local Similarity 45.6%; Pred. No. 0.00047; length 3127;  
 Matches 194; Conservative 0; Mismatches 231; Indels 0; Gaps 0;

Qy 505 CTCGAAAGCAGATGAAAGTACTCTAGACGAGCACAGATGAGACCAACACACAGAG 564  
 Db 1738 CAGCAGGATGAGCAGCAGCAGATGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGGAG 1797

Qy 565 GAGGGGGGGGGGTCAAGGAGCAAGATGAGACCATGGAGCAGATGAGCTCTACTCCAG 624  
 Db 1798 GAGCAGGAGCAGCAGGAGGAGGAGGAGCAGGAGTTAGAGGAGCAGGAGCTAGAG 1857

Qy 625 AGCCAGCTTCCCTGAGGGAGGAGATATCCGAGATGGGTTGGAGCAGTCAGGGTG 684  
 Db 1858 GACGAGGAGCAGGAGTTAGAGGAGCAGGAGCAGGAGCAGGAGCAGGAGGAGTTA 1917

Qy 685 GACACGCTGGCTGTGACTGTGTCCTCACAAAGAGTACCGAGAATCTAAAGGCC 744  
 Db 1918 GAGGAGCAGGAGCAGGAGGTAGAGGAGCAGGAGCTAGAGCAGGAG 1977

Qy 745 CGGAGGGCTCAGGGAGGTGGCTGACAGCAGTGGAGGAGTTAGAGGAGCAGGAGCAG 804  
 Db 1978 TTTAGAGGAGCAGGAGCAGGAGTTAGATCAGCAGGAGCAGGAGCTAGAGGAGGAGCAG 2037

Qy 805 AGCTTGAGCAGCTACTCTGATGATGATGGCCAGTGTAGACGAGTCAGCCAG 864  
 Db 2038 GACTTAGAGGAGCAGGAGCAGGAGTTAGAGGAGCAGGAGCAGGAGTTAGAGGAGCAG 2097

Qy 865 AGGGACTTACAGAGTGTGCTGACAGAAATCATGAGCTGAAGAAAGCTAAGATGCTG 924  
 Db 2098 CAGGAGTTAGAGCAGGAGCAGGAGTTAGAGGAGCAGGAGCAGGAGTTAGAGGAGCAG 2157

Qy 925 CAGGA 929  
 Db 2158 GACCA 2162

RESULT 34

AC098712 AC098712 207683 bp DNA linear HTG 14-NOV-2001  
 DEFINITION MUS musculus chromosome UNK clone RP23-2A21, WORKING DRAFT  
 ACCESSION AC098712  
 VERSION AC098712.2 GI:16924164  
 KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT; HTGS\_ACTIVEFIN.  
 SOURCE  
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 20763)  
 McPherson, J.D. and Waterston, R.H.  
 JOURNAL unpublished  
 REFERENCE 2 (bases 1 to 20763)  
 McPherson, J.D. and Waterston, R.H.  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT Submitted (31-OCT-2001) Genome Sequencing Center, 4444 Forest Park  
 Parkway, St. Louis, MO 63108, USA  
 On Nov 14, 2001 this sequence version replaced gi:16554409.

----- Genome Center: -----  
 Center: Washington University Genome Sequencing Center  
 Center code: WUDSC  
 Center web site: http://genome.wustl.edu/gsc/index.shtml  
 Contact: submissions@wustl.edu  
 ----- Project Information -----  
 Center project name: M\_BA002421  
 ----- Summary Statistics -----  
 Sequencing vector: M13; %

Chemistry: Dye-Primer ET; % of reads  
 Chemistry: dye-terminator Big Dye; % of reads  
 Assembly program: Phrap; version 0.99319  
 Consensus quality: 205930 bases at least Q40  
 Consensus quality: 206594 bases at least Q30  
 Consensus quality: 207083 bases at least Q20  
 Insert size: ; agarose-fp  
 Insert size: 219554; sum-of-contigs  
 Quality coverage: 25.41 in Q20 bases; agarose-fp  
 Quality coverage: 24.42 in Q20 bases; sum-of-contigs

\* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 5 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.  
 \* 1 1240: contig of 1240 bp in length  
 \* 1241 1340: gap of unknown length  
 \* 1341 1429: contig of 12889 bp in length  
 \* 14230 14329: gap of unknown length  
 \* 14330 3981: contig of 25472 bp in length  
 \* 39802 39901: gap of unknown length  
 \* 39902 39902: contig of 31779 bp in length  
 \* 71680 71680: gap of unknown length  
 \* 71781 71781: contig of 135903 bp in length.  
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 /db\_xref="taxon:10900"  
 /chromosome="UNK"  
 /clone="RP23-2A21"  
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 1..14229  
 14330..39801  
 /note="assembly\_name:Contig37"  
 39902..71680  
 1..1240  
 misc\_feature  
 /note="assembly\_name:Contig38"  
 71781..207683  
 /note="assembly\_name:Contig39"  
 BASE COUNT 62336 a 44191 c 44243 g 56460 t 453 others  
 ORIGIN

Query Match 2.8%; Score 55.4; DB 2; Length 207683;  
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 Matches 215; Conservative 0; Mismatches 266; Indels 0; Gaps 0;

Qy 305 AGGAGGAGGAGATGTCCTGGATGAGATACTCTAAAGATGACTGACATGTCAGAG 364  
 Db 186130 AGGAGCAGGAGCAGGAGGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGC 186189  
 Qy 365 CCCAGCTTCCAGAAAGCAAGGAGAAAGACAGCAGCAGCAGTCATCCACACTCTGC 424  
 Db 186190 AGGAGGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGC 186249

Qy 425 GGATACCTGGAGAACGCAATGCTACTGTGATCTCGCAGCAGCCTGGCAGG 484  
 Db 186250 AGGAGGAGGAGGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGC 186309

Qy 485 CCCAGATCTGGCTCCACACTGAAAGCAGATGAAAGTACTTAGCAGCAGCAGGATG 544  
 Db 186310 AGGAGGAGGAGGAGGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGC 186369

Qy 545 AGACACACACACACACAGAGGAGCAGGAGCAGGAGCAGGAGCAGGAGGAGGAGGAGC 604  
 Db 186370 AGGAGGAGGAGGAGGAGCAGGAGCAGGAGCAGGAGGAGGAGGAGGAGGAGGAGC 186429

Qy 605 AGATTGAGCTTCTACTCCAGAGGCCAGTCCTCAGGAGGAGGAGGAGGAGCAGATGG 664





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  /rpt_family="MIR"
repeat_region 21830 . 21872
  /rpt_family="AT_rich"
repeat_region 21957 . 22257
  /rpt_family="Alus"
repeat_region complement(2438..22338)
  /rpt_family="MLTBJ"
repeat_region complement(23375..23667)
  /rpt_family="Aluy"
repeat_region 21553 . 24858
  /rpt_family="Aluy"
repeat_region complement(25021..25334)
  /rpt_family="MIR"
repeat_region 24957 . 27261
  /rpt_family="MLTIB"
repeat_region complement(27524..27669)
  /rpt_family="Aluy"
repeat_region complement(27670..27964)
  /rpt_family="Alusp"
repeat_region complement(27965..28210)
  /rpt_family="MLTIB"
repeat_region complement(28228..28522)
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repeat_region complement(28592..28700)
  /rpt_family="MIR"
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  /rpt_family="MIR"
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  /rpt_family="MIR"
repeat_region 30227 . 30267
  /rpt_family="TGJ"
repeat_region 30276 . 30321
  /rpt_family="(CA)n"
repeat_region complement(30322..30611)
  /rpt_family="Alujo"
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repeat_region 32028 . 32107
repeat_region /rpt_family="L1PA4"
repeat_region complement(32919..33182)
  /rpt_family="MIR"
repeat_region 34169 . 34334
  /rpt_family="CT-rich"
repeat_region 34774 . 35007
  /rpt_family="MIR"
repeat_region 35589 . 35621
  /rpt_family="AT_rich"
repeat_region 35763 . 36142
  /rpt_family="MER41A"
repeat_region 36143 . 36652
  /rpt_family="Alusg"
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repeat_region 38011 . 38071
  /rpt_family="CT-rich"
repeat_region 38083 . 38262
  /rpt_family="(TTC)n"
repeat_region 38235 . 38319
  /rpt_family="(TTC)n"
repeat_region 38320 . 38499
  /rpt_family="(TTC)n"

Query Match 2.7%; Score 53.8; DB 9; Length 180385;
Best Local Similarity 44.5%; Pred. No. 0.0023; Mismatches 267; Indels 0; Gaps 0;
Matches 214; Conservative 0; Mismatches 267; Indels 0; Gaps 0;

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RESULT 38

AL589661	AL589661	241432 bp	DNA	linear	ROD	30-JAN-2002
LOCUS	AL589661	Mouse DNA sequence from clone Rp23-58B7 on chromosome 15.				
DEFINITION	AL589661					
ACCESSION	AL589661.21					
VERSION	61:18476659					
KEYWORDS	HTG.					
SOURCE	house mouse.					
ORGANISM	Mus musculus					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 241432)					
AUTHORS	Dunn, M.					
TITLE	Direct Submission					
JOURNAL	Submitted (30-JAN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: clone@sanger.ac.uk humquery@sanger.ac.uk Clone requests: clone@clone@sanger.ac.uk					
COMMENT	<p>On Feb 1, 2002 this sequence version replaced 61:18151481. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.</p> <p>This sequence was finished as follows: unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e. phred quality &gt; 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EML; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at <a href="http://www.sanger.ac.uk/Projects/C_elegans/wormpep">http://www.sanger.ac.uk/Projects/C_elegans/wormpep</a> Rp23-58B7 is</p>					

FEATURES	source	Query Match, Best Local Similarity, Matches	Score, Pred. No., Mismatches	Length, Indels, Gaps	Location/Qualifiers
misc_feature		305 AGGAGGAGGAGAMGTCTTGTGAGATTCTTAAGAATGAACTGACATGTCAGAG 147938	2.7%; 47.4%; 228; 0;	Score 53.8; DB 10; Length 241432; Pred. No. 0.0024; Mismatches 247; Indels 6; Gaps 2;	1. -241432 /organism="Mus musculus" /db_xref="taxon:10090" /chromosome="15" /clone="RP23-58B7" /clone.lib="RPCI-23" /note="Sequence from uni-directional dgtp big dye terminator reads only." /note="Sequence from uni-directional dgtp big dye terminator reads only."
BASE COUNT	ORIGIN	64293 a	50995 c	55888 g	70256 t
REFERENCE		Qy 425 GGATACCTGGAGAACGAACTGACTGTGGATCTGGCCCTGGGCAGG 147811	4.7%; 47.4%; 228; 0;	Score 53.8; DB 10; Length 241432; Pred. No. 0.0024; Mismatches 247; Indels 6; Gaps 2;	2 (bases 1 to 195294)
AUTHORS	McCombie, W.R.	Db 147872 AGGAGGAGCAGGGAGGGAGGAGCAGGGAGGAGGAGGAGGAGG 147931	4.7%; 47.4%; 228; 0;	Score 53.8; DB 10; Length 241432; Pred. No. 0.0024; Mismatches 247; Indels 6; Gaps 2;	McCombie, W.R.
JOURNAL		Qy 485 CCCAGATCTGCTCCACACTGAAAGACAGGAGGACCCAGTCATCGACACTGTC 424	2.7%; 47.4%; 228; 0;	Score 53.8; DB 10; Length 241432; Pred. No. 0.0024; Mismatches 247; Indels 6; Gaps 2;	
COMMENT		Db 147812 ARAGAGGAGGAGGAGCAGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 364	2.7%; 47.4%; 228; 0;	Score 53.8; DB 10; Length 241432; Pred. No. 0.0024; Mismatches 247; Indels 6; Gaps 2;	
AUTHORS	McCombie, W.R.	Db 147932 AGGAGGAGCAGGGAGGAGCAGGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 147991	2.7%; 47.4%; 228; 0;	Score 53.8; DB 10; Length 241432; Pred. No. 0.0024; Mismatches 247; Indels 6; Gaps 2;	
JOURNAL		Qy 545 AGCCAAACAGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 604	2.7%; 47.4%; 228; 0;	Score 53.8; DB 10; Length 241432; Pred. No. 0.0024; Mismatches 247; Indels 6; Gaps 2;	
COMMENT		Db 147992 AGGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 148045	2.7%; 47.4%; 228; 0;	Score 53.8; DB 10; Length 241432; Pred. No. 0.0024; Mismatches 247; Indels 6; Gaps 2;	
AUTHORS	McCombie, W.R.	Qy 605 AGATTGAGCTCTACTCCAGAGCAGTCCTCTAGGGTGGAGATGCCGACATGG 664	2.7%; 47.4%; 228; 0;	Score 53.8; DB 10; Length 241432; Pred. No. 0.0024; Mismatches 247; Indels 6; Gaps 2;	
JOURNAL		Db 148046 AGGAGGAGGAGGAGCAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 148105	2.7%; 47.4%; 228; 0;	Score 53.8; DB 10; Length 241432; Pred. No. 0.0024; Mismatches 247; Indels 6; Gaps 2;	
COMMENT		Qy 655 GTCGTGGACAGTCAGCGGTGGAAACAGCTGGCTGTACTGTGGTCTCTCAAGAAAGT 724	2.7%; 47.4%; 228; 0;	Score 53.8; DB 10; Length 241432; Pred. No. 0.0024; Mismatches 247; Indels 6; Gaps 2;	
AUTHORS	McCombie, W.R.	Db 148106 AGGAGGAGCAGGAGCAGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 148165	2.7%; 47.4%; 228; 0;	Score 53.8; DB 10; Length 241432; Pred. No. 0.0024; Mismatches 247; Indels 6; Gaps 2;	
JOURNAL		Qy 725 ACCAGAACCTAAAGAGGAGCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 784	2.7%; 47.4%; 228; 0;	Score 53.8; DB 10; Length 241432; Pred. No. 0.0024; Mismatches 247; Indels 6; Gaps 2;	
COMMENT		Db 148166 AGGAGGAGCAGGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 148225	2.7%; 47.4%; 228; 0;	Score 53.8; DB 10; Length 241432; Pred. No. 0.0024; Mismatches 247; Indels 6; Gaps 2;	
AUTHORS	McCombie, W.R.	Qy 785 A 785	2.7%; 47.4%; 228; 0;	Score 53.8; DB 10; Length 241432; Pred. No. 0.0024; Mismatches 247; Indels 6; Gaps 2;	
JOURNAL		Db 148226 A 148226	2.7%; 47.4%; 228; 0;	Score 53.8; DB 10; Length 241432; Pred. No. 0.0024; Mismatches 247; Indels 6; Gaps 2;	
COMMENT		RESULT 39	2.7%; 47.4%; 228; 0;	Score 53.8; DB 10; Length 241432; Pred. No. 0.0024; Mismatches 247; Indels 6; Gaps 2;	
DEFINITION	Mus musculus clone RP23-41205, WORKING DRAFT SEQUENCE, 17 unordered pieces	AC051623	195294 bp	DNA linear	HTG 06-SBP-2000
ACCESSION		AC051623			
VERSION	AC051623.4	AC051623.4	GI:9972322		
KEYWORD	HTGS_PHASE1, HTGS_DRAFT				
SOURCE	house mouse				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Rodentia; Sciurognath; Muridae; Murinae; Mus. (bases 1 to 195294)	1			
FEATURES	source	Query Match, Best Local Similarity, Matches	Score, Pred. No., Mismatches	Length, Indels, Gaps	Location/Qualifiers
REFERENCE		Qy 182161 182299 gap of unknown length	2.7%; 47.4%; 228; 0;	Score 53.8; DB 10; Length 241432; Pred. No. 0.0024; Mismatches 247; Indels 6; Gaps 2;	1. -182299 /organism="Mus musculus" /db_xref="taxon:10090" /clone="RP23-41205"
AUTHORS	McCombie, W.R.	Db 182300 182300	2.7%; 47.4%; 228; 0;	Score 53.8; DB 10; Length 241432; Pred. No. 0.0024; Mismatches 247; Indels 6; Gaps 2;	
JOURNAL		Qy 182279 182279	2.7%; 47.4%; 228; 0;	Score 53.8; DB 10; Length 241432; Pred. No. 0.0024; Mismatches 247; Indels 6; Gaps 2;	
COMMENT		Db 182418 182418	2.7%; 47.4%; 228; 0;	Score 53.8; DB 10; Length 241432; Pred. No. 0.0024; Mismatches 247; Indels 6; Gaps 2;	
AUTHORS	McCombie, W.R.	Qy 182253 182253	2.7%; 47.4%; 228; 0;	Score 53.8; DB 10; Length 241432; Pred. No. 0.0024; Mismatches 247; Indels 6; Gaps 2;	
JOURNAL		Db 182392 182392	2.7%; 47.4%; 228; 0;	Score 53.8; DB 10; Length 241432; Pred. No. 0.0024; Mismatches 247; Indels 6; Gaps 2;	
COMMENT		Qy 191031 191031	2.7%; 47.4%; 228; 0;	Score 53.8; DB 10; Length 241432; Pred. No. 0.0024; Mismatches 247; Indels 6; Gaps 2;	
DEFINITION	Mus musculus clone RP23-41205, WORKING DRAFT SEQUENCE, 17 unordered pieces	AC051623	193703 contig of 2534 bp in length	DNA linear	HTG 06-SBP-2000
ACCESSION		AC051623	193704 193704		
VERSION	AC051623.4	AC051623.4	193842 gap of unknown length		
KEYWORD	HTGS_PHASE1, HTGS_DRAFT				
SOURCE	house mouse				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Rodentia; Sciurognath; Muridae; Murinae; Mus. (bases 1 to 195294)	1			
FEATURES	source	Query Match, Best Local Similarity, Matches	Score, Pred. No., Mismatches	Length, Indels, Gaps	Location/Qualifiers
REFERENCE		Qy 48944 48944	2.7%; 47.4%; 228; 0;	Score 53.8; DB 10; Length 241432; Pred. No. 0.0024; Mismatches 247; Indels 6; Gaps 2;	1. -48944 /organism="Mus musculus" /db_xref="taxon:10090" /clone="RP23-41205"
AUTHORS	McCombie, W.R.	Db 48556 48556	2.7%; 47.4%; 228; 0;	Score 53.8; DB 10; Length 241432; Pred. No. 0.0024; Mismatches 247; Indels 6; Gaps 2;	
JOURNAL		Qy 46839 46839	2.7%; 47.4%; 228; 0;	Score 53.8; DB 10; Length 241432; Pred. No. 0.0024; Mismatches 247; Indels 6; Gaps 2;	
COMMENT		Qy 48701 48701	2.7%; 47.4%; 228; 0;	Score 53.8; DB 10; Length 241432; Pred. No. 0.0024; Mismatches 247; Indels 6; Gaps 2;	
DEFINITION	Mus musculus				
ACCESSION					
VERSION					
KEYWORD					
SOURCE					
ORGANISM					
REFERENCE					



Db 201716 GCAAGGAGGAGGAGGAGGAGAAGAAGAAGGAGGAGGAGGAGGAGGAGA 201775  
Qy 627 CCGCTCCTGAGGTGGAGGACATGATCCGACACATGGTGGGACAGTCAGGGTGA 686  
Db 201776 GAGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA 201835  
Qy 687 ACAGCTTGCTGTGACTGTGCTCTCAAGAAAGACTACGAACTAAAGGCCACG 746  
Db 201836 GGAGGAGGAGGAGGAGGAGGAGGAAAGGAGGAGGAGGAGGAGGAGGAGGA 201895  
Qy 747 GAGGCCCTCAGGGAGGTGGCTCACACAGCTGGAGAGGA 785  
Db 201896 GAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA 201934

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Job time: 15451 sec

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